						1
PDB annotation	HYDROLASE OCCUPATION OF THE MICROPLASMINOGEN, SERINE PROTEASE, ZYMOGEN, CHYMOTRYPSIN 2 FAMILY, HYDROLASE	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS		
Coumpound	PLASMINOGEN; CHAIN: A, B, C, D;	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDAT E (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	HYDROLASE (SERINE PROTEINASE) TRYPSIN
SEQFOL D score	117.30		97.78			100.94
PMF		1.00		1.00	1.00	
Verify score		0.65	·	0.45	0.79	
Psi Blast	3.4e-71	3.4e-72	3.4e-72	1.7e-78	5.1e-80	5.1e-80
END	239	239	240	239	239	240
STAR T AA	12	30	30	30	30	30
CHA1 N ID	¥ •	ව	Ð	В	A	¥
PDB ID	lqrz	lsgf	1sgf	lslw	ltm	141
SEQ ID NO:	1464	1464	1464	1464	1464	1464

				LASE, JON, GNAL	LASE, TON, GNAL	GNAL	GNAL		
PDB annotation				SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAI	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAI	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	COMFLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION	COMPLEX (SIGNAL
Coumpound	(E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DISOPROPYL-FLUOROPHOSPHOFLUORIDAT E (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	BETA TRYPSIN; CHAIN: NULL;	BETA TRYPSIN; CHAIN: NULL;	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	14-3-3 PROTEIN ZETA; CHAIN:
SEQFOL D score			97.32		99.14	234.97			284.35
PMF		1.00		1.00			1.00	1.00	
Verify score		0.65		0.73			0.55	0.59	
Psi Blast		5.1e-79	5.1e-79	1.7e-76	1.7e-76	1.7e-98	1.7e-98	0	0
END AA		237	239	239	239	229	230	232	232
STAR T AA		30	30	30	30	ε	£	Е	60
CHAI N ID						∢	¥	∢	A.
PDB ID		2tbs	2tbs	5ptp	Sptp]a4o	1a4o	igi e	lqja
SEQ ID NO:		1464	1464	1464	1464	1470	1470	1470	1470

PDB annotation	TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION		TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN	-	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	-		HELICAL LINKER REGION, 22	STRICTINAL PROTEIN	†	A, STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COLLED-COILS,	+		KDA PROTEIN, P35A, THREE HELIX	BUNDLE	-	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	
Coumpound	A, B; PHOSPHOPEPTIDE; CHAIN: Q, R		COLICIN IA; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A,		-	ALPHA SPECTRIN; CHAIN: A,	ပ်မျိ			. In the same and the same	ALPHA SPECTRIN; CHAIN: A, B, C;			SYNTAXIN-1A: CHAIN: A. B. C.				SYNTAXIN-1A; CHAIN: A, B, C;			HUMAN SKELETAL MUSCLE
SEQFOL D score		1	133.38											w.ee.vo.			٠					
PMF score				0.03			-0.17				900	6.0			-0.13				-0.15			0.11
Verify score				-0.15	i		0.12				200	c0:0			0.19				0.01			0.02
Psi Blast			3.4e-08	6e-15			7.5e-16				00.00	3e-20			1.5e-09				4.5e-08			6e-19
END			621	322			363				070	248			139				214			426
STAR T AA		•	48	117			152				٥٢	×			23				95	·		196
CHAI N ID				¥			A					₹			\ ∀				∢			A
PDB ID	·		1cii	Icun			lcun					Icnu			lez3				lez3			1quu
SEQ ID NO:			1471	1471			1471					1471			1471	nana ka			1471			147[

PDB annotation	CONTRACTILE PROTEIN	HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION	MOITEI GOSKA ett.) VET IMMOO	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	ANKYRIN 2 REPEAT HELIX	STRUCTURAL PROTEIN TWO	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELLY COLLED-COLES,	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COLLED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN ALPHA	HELICAL LINKER REGION, 22 TANDEM 3-HELIX COLLED-COLLS.	
Coumpound	THE STEEL THE ST	ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	NE VADBA B BKS: CHARL: A C:	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,		ALPHA SPECTRIN; CHAIN: A,	် ရ			ALPHA SPECTRIN; CHAIN: A,	B, C;			ALPHA SPECTRIN: CHAIN: A.	် ကိ				ALPHA SPECTRIN; CHAIN: A,	ĵ ĵ	
SEQFOL D score																							
PMF score	6	-0.02	0.03	200	₫ 5 5			0.15				0.19				0.55					0.35		
Verify score	000	0.09	-0.11	750	-0.56			-0.18				-0.12				-0.05					0.19		
Psi Blast	1 5 15	1.56-15	6e-0 9	2000	0.0045			3e- 06				9e-13				1.5e-15					4.5e-15		
END	707	784	307	Ę	<u> </u>			337				458	-		****	687					724		
STAR T AA	l i	217	32	[73			150				241			maner	460					206		
CHAI N ID		∢		t	ъ			A				Ą				\ \ \	•				∢		
PDB ID		Iquu	1sig		<u> </u>			1cun				1cun				1cun					lcun		
SEQ U		1471	1471		1475			1476				1476				1476) :				1476		

PDB annotation	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22	TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELLOGONED-COILS,	SIKUCIUKAL PKUIEIN	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35
Coumpound		ALPHA SPECTRIN; CHAIN: A, B, C;		ALPHA SPECTRIN; CHAIN: A,	် ပို့		ALPHA SPECTRIN; CHAIN: A,	B; Ç;				SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;				SYNTAXIN-1A; CHAIN: A, B, C;
SEQFOL D score								•			i																	·
PMF		0.42		60:0			-0.14					-0.05			0.01			90.0	,		0.03			0.03				-0.06
Verify score		0.15		0.08			-0.00					0.03			-0.30			-0.21	,,,,,		-0.19			-0.26				0.00
Psi Blast		9e- 17		1.2e-13			6e-12					6e-16			1.5e-16			6e-18			6e-13			3e-07	•		منده م	1.5e-11
END		794		850			916					423			597			711			911			363				719
STAR T AA		583		632			721					216			380			503			700			256				593
CHAI		¥	,	A			4					В			В			В			B			¥				Ą
PDB ID		lcun		1cun		÷ (Icun			-		1dn1			1dn1			1dn]			1dn]			1ez3				lez3
SEQ ID		1476		1476			1476					1476			1476			1476			1476			1476				1476

PDB annotation	KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN		IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN,
Coampound		SYNTAXIN-1A; CHAIN: A, B, C;	SSOI PROTEIN; CHAIN: A;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	NEURO-ONCOLOGICAL VENTRAL ANTIGEN 1; CHAIN: A;	RNA-BINDING			
SEQFOL D score					-			. •			
PMF score		0.19	0.15	0.59	0.00	0.06	0.54	0.21	0.12	0.82	0.96
Verify score	-	0.28	0.17	-0.29	-0.19	-0.29	-0.02	0.07	-0.07	0.62	0.19
Psi Blast		4.5e-10	9e-10	0.0001	4.5e-22	3e-26	6e-24	1.5e-24	0.00017	0.00015	0.00075
END		822	648	711	573	640	749	790	555	199	567
STAR T AA		704	491	548	320	390	480	528	464	609	609
CHAI N ID		¥	Α	U	4	∢	Ą	A	∢	4	Ą
PDB ID		lez3	1ffo	1fxk	Iquu	1quu	lquu	Iguu	Ises	1dt4	1dtj
SEQ ID NO:		1476	1476	1476	1476	1476	1476	1476	1476	1479	1479

PDB annotation	ALPHA-BETA FOLD RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP:GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION	RNA BINDING PROTEIN/RNA ASTROCYTIC NOVA-LIKE RNA- BINDING PROTEIN; KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF, PROTEIN/RNA 2 STRUCTURE	RNA BINDING PROTEIN KH3; HNRNP K, KH DOMAIN, THREE- DIMENSIONAL STRUCTURE, NMR,
Coumpound	NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	RNA-BINDING PROTEIN NOVA-2; CHAIN: A, B; 20-MER RNA HAIRPIN; CHAIN: C, D;	HNRNP K; CHAIN: A;
SEQFOL D score							
PMF score		0.94	68.0	1.00	1.90	0.72	0.36
Verify score		0.59	0.60	0.75	0.49	0.50	0.36
Psi Blast			1e-05	0 .	0	0.00014	0.0014
END		667	1999	613	739	675	671
STAR T AA		609	609	ريا د	15	609	610
CHAI		Ų	Д	∢	∢	∢	4
PDB ID		14tj	1dtj	le3h	le3p	Jec6	1khm
SEQ U		1479	1479	1479	1479	1479	1479

SEQ NO ID	PDB ID	CHA1 N ID	STAR	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										C-MYC, 2 DIPOLAR COUPLING, DNA-BINDING, RNA-BINDING, RNA BINDING 3 PROTEIN
1479	1sro		675	751	5.1e-21	0.78	1.00		PNPASE; CHAIN: NULL;	SI RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, S1
										RNA-BINDING DOMAIN, POLYNUCLEOTIDE PHOSPHORYLASE 2 (PNPASE)
1479	lvig		603	299	1e-06	0.46	0:30	-	VIGILIN; IVIG 5 CHAIN: NULL; IVIG 6	RIBONUCLEOPROTEIN RNA- BINDING PROTEIN IVIG 19
1480	1d9x	¥	442	528	1.7e-06	-0.14	0.00		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1480	X6P1	A	447	602	600.0	-0.21	0.03		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1480	1fina	∢	427	492	0.00015	-0.14	0.54	- 4.	CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1480	1qhg	¥	444	524	1.5e.11	-0.19	0.83		PCRA (SUBUNIT); CHAIN: A; PCRA (SUBUNIT); CHAIN: B; PCRA (SUBUNIT); CHAIN: C; PCRA (SUBUNIT); CHAIN: D;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, ATP- 2 BINDING, DNA- BINDING
										•
1484	laoa		4	122	6.8e-26	0.28	0.96		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORYLATION
1484	1dxx	∢	7	120	5.1e-28	0.54	0.68		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN- BINDING, UTROPHIN

	4 € 🖼	 	<u> </u>	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
lqag A		v	121	3.4e-26	0.33	0.39		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
11f6 A	ı	998	953	0.0045	-0.10	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
4	1 1	873	926	0.00045	0.08	0.41		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1bor	j	339	377	0.0001	-0.38	0.00		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1chc	1	336	378	3.4e-10	-0.35	0.29		VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
lfbv A		336	381	5.1e-09	-0.24	0.15		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGÁSE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION CARROCENE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1g25 A	1	336	387	5.1e-06	0.26	0.62		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1;	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING

PDB annotation	FINGER (C3HC4)	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING	PROTEIN 1; RAG1, V(D)J	RECOMBINATION, ANTIBODY,	MAD, RING FINGER, 2 ZINC	BINUCLEAR CLUSTER, ZINC	FINGER, DINA-BINDING FROI BIN	HEXAMERIZATION DOMAIN	HEXAMERIZATION DOMAIN.	ATPASE, TRANSPORT	CHAPERONE HSLV; HSLU	CHAPERONE, HSLVU, CLPQY, AAA-	ATPASE, ATP-DEPENDENT 2	PROTEOLYSIS, PROTEASOME	CHAPERONE HSLV; HSLU	CHAPERONE, HSLVU, CLPQY, AAA-	TPASE, ATP-DEPENDENT 2	PROTEOLYSIS, PROTEASOME	HYDROLASE ARSA ATPASE; P-	LOOP, ANTIMONITE BINDING SITE,	IF DINDING SILE	CELL CYCLE CDCOP; CDC6, CDC18,	ORCI, AAA PROIEIN, DNA	KEPLICATION INITATION 2	FACTOR, CELL CYCLE CONTROL	FACTOR	CHAPERONE AAA-ATPASE, CLPY,	AIP-DEPENDENT PROTEOLYSIS	CHAPERONE AAA-ATPASE, CLPY,	THE PREPARE OF STATES AND THE PERSON OF THE	IRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP,
Coumpound	CHAIN: A;	RAGI; CHAIN: NULL;	ndq	-				N-ETHYLMALEIMIDE.	OTEN:		HSLV;			CHAIN: E, F;	HSLV;		FIN HSLU;		ARSENITE-TRANSLOCATING F	ATPASE; CHAIN: A;			FROIEIN 6; CHAIN: A, B;			_	OCK PROTEIN HSLU;	7	HEAT SHOCK PROTEIN HSLU; CHARL.	+	SHIKIMATE KINASE; CHAIN: 1 A, B;
SEQFOL D score																											,		٠.		·
PMF score		0.06						-0.18	}		-0.13				50.0				0.28		0.45	0.45		_		, ,	0.94		0.04	0, 0	U.49
Verify score		0.10						0.11			0.01	,			-0.20				-0.39		35.0	0.15				,,,,	0. 4 0	,	-0.11	63.0	-0.33
Psi Blast		3.4e-09						1.2e-11			8.5e-12				1.5e-12				0.0015		10.	1.2e-15				50	1.26-37		1.2e-17	1 50 05	1.36-03
END		387						782			434				634				514		983	629				5	660	[618	206	390
STAR T AA		320						626			339				339				83	-	24.4	¥_				000	250	3	339	3,60	203
CHAI N ID								A			ਜ				щ				• «			₫.					∢		∢		4
PDB ID		1rmd		_				1d2n			1e94				1694				1f48		4]	1841		1g41	10,1	ISUK
SEQ ID NO:		1487						1490			1490				1490				1490		5	1490				50,	2×41	,	1490	1400	1490

PDB annotation	SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE	PROTEIN TRANSPORT FIFTY-FOUR HOMOLOG, P48; FFH, SRP54, SIGNAL RECOGNITION PARTICLE, GTPASE, M DOMAIN, 2 RNA-BINDING, SIGNAL SEQUENCE-BINDING, HELIX-TURN-HELIX, 3 PROTEIN TARGETING, PROTEIN TRANSPORT	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	TRANSCRIPTION RNAIP; RANGAP;	GTPASE-ACTIVATING PROTEIN	FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP.	LRR, LEUCINE- 2 RICH REPEAT	PROTEIN, TWINNING,	HEMIHEDRAL TWINNING, 3	MEROHEDRAL TWINNING, MEROHEDRY	ACETYLATION RNASE INHIBITOR,	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION,	LEUCINE-RICH REPEATS	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
Coumpound	-	FFH; CHAIN: A, B, C;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	GTPASE-ACTIVATING	PROTEIN RNA1_SCHPO;	CHAIN: A, B;					RIBONUCLEASE INHIBITOR;	CHAIN: NOEL;		LITHOSTATHINE; CHAIN: NULL
SEQFOL D score														
PMF score		0.01	0.94	0.18							0.65			1.00
Verify score		-0.24	0.10	0.03							0.33			0.82
Psi Blast		1e-0 <i>5</i>	1.5e-48	6.8e-27						. A Conf Combad	3.4e-43			 1e-42
END AA		537	394	168							393			166
STAR T AA		347	178	841					,		178			 36
CHAI N ID	,	¥	A •	Ą										
PDB ID			 1a4y	lyrg							2bnh			Hit.
SEQ ID NO:		1490	1491	1491							1491			1495

PDB CHAI STAR ID NID TAA	STAR T AA		END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
36 166		166		7.5e-43	0.82	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
36 166		166		7.5e-43			212.11	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1qdd A 23 166		991		1e-44	0.77	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1qdd A 23 166		166		6e-47	0.77	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1qdd A 23 166		166	· ·	6e-47			226.04	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
lqqe A 489 634	634		1	1.le-13	0.14	-0.17		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX- TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
A 1 713	1 713	713		0	-0.16	0.46		CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	HYDROLASE SERCA1; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT
1c4o A 393 540		540		1e-12	0.20	0.96		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
1c4o A 448 516		516		1.4e-19	-0.10	0.83		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC,

TVIII.

PDB annotation	HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	GENE REGULATION APO PROTEIN	GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF4A, HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF4A, HELICASE, DEAD-BOX PROTEIN	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE	GENE REGULATION EIF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY	HELICASE RNA HELICASE, HEPATITIS C VIRUS, HCV, UNWINDING MECHANISM	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN
Coumpound	CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	HCV HELICASE; CHAIN: A, B;	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	RNA HELICASE; CHAIN: NULL	PROTEIN KINASE C (BETA); CHAIN: A, B;
SEQFOL D score												77.04
PMF score		0.19	0.80	0.09	0.76	0.86	1.00	1.00	0.22	00'1	0.04	
Verify		-0.57	0.17	-0,16	0.39	0.26	0.83	0.47	-0.18	0.55	-0.59	
Psi Blast		0.00068	8.5e-13	9e-29	3.4e-16	1.2e-43	3.4e-59	0	0.0003	5.1e-56	1.5e-53	9e-25
END		223	540	531	528	558	340	558	325	340	522	137
STAR T AA		144	393	258	380	376	127	127	158	127	158	12
CHAI		Ą	¥	Ą	¥	¥	A	В	K	Ą		4
PDB ID		1d2m	1d2m	1d9x	1d9x	1fuk	1fuu	Ifuu	Ihei	lqde	8ohm	1a25
SEQ NO:		1499	1499	1499	1499	1499	1499	1499	1499	1499	1499	1502

PDB annotation	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCTUM-BINDING PROTEIN CALB; CALCTUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCTUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLA2. PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
Соитропид	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
SEQFOL D score				·				
PMF score	0.54	1.00	0.90	0.35	0.10	0.65	0.45	0.24
Verify score	-0.05	0.42	0.62	0.04	0.36	0.07	0.29	0.34
Psi Blast	1.5e-26	9e-25	1.46-24	3.4e-30	1.7e-28	1.3e-29	7.5e-24	3.4e-22
END AA	287		117	287	122	338	184	302
STAR T AA	167	17	18	167	61	184	22	183
CHAI N ID	Ą	V	¥	A	A	¥	¥	¥
PDB ID	1a25	1a25	1a25	Ibyn	1byn	1cjy	1cjy	ldjx
SEQ NO:	1502	1502	1502	1502	1502	1502	1502	1502

PDB annotation	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROI ASP 17PID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING, PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-DI;	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE OF PHOSPHOLIPE SPECIFIC	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING PROTEIN,	PHOSPHATTDYI SERINE PROTEIN	KINASE C	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	KINASE C	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	KINASE C	HYDROLASE CALB DOMAIN;	HYDROLASE, C2 DOMAIN, CALB DOMAIN	HYDROLASE CALB DOMAIN;
Coumpound		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B.	a			PHOSPHOINOSITIDE-SPECIFIC PHOSPHOI IPASE C CHAIN: A	B;		*.		PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;			PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;				PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;			PHOSPHOLIPASE A2: CHAIN:	NULL;	PHOSPHOLIPASE A2; CHAIN:
SEQFOL D score																										51.76
PMF score		0.16				0.21					1.00				0.07				,	0.88				0.28		
Verify		0.49				0.20					0.52		-		-0.13				,	0.47				0.17		
Psi Blast		6.8e-23				3.4e-22					1e-24				5.1e-28					6.8e-27				6e-23		4.5e-25
END		121				302					137				295				,	117				276		145
STAR		27				183					17				183					∞.				184		20
CHAI N ID		∢				8					A •				¥				_ .	¥						
PDB ID		1djx				1djx					Idsy				Idsy					ldsy				Irlw		lrlw
SEQ ID NO:		1502				1502					1502				1502					1502				1502		1502

PDB annotation	HYDROLASE, C2 DOMAIN, CALB DOMAIN	HYDROLASE CAEB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN				ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA!; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION
Соитроия	NULL;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (PIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOL, PID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;	SYNAPTOTAGMIN III; CHAIN: A;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA;
SEQFOL D score					59.11				
PMF score		0.93	0.48	0.21		0.34	0.19	1.00	0.96
Verify score		0.78	0.18	0.36		0.00	-0.57	0.40	0.29
Psi Blast		4.5e-25	3.4e-30	1.7e-28	1.7e-28	1.2e-26	6.8e-53	1.5e-26	1.2e-29
END		143	284	122	130	294	223	861	828
STAR T AA		30	167	61	2	168	144	693	694
CHAI N ID		•				¥		m	В
PDB		Irlw	Irsy	Irsy	Irsy	3rpb		Тамс	lawc
SEQ	2	1502	1502	1502	1502	1502	1502	1503	1503

																						,		\neg
PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANK YKIN KEPEAIS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPHETA1: COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TE ANSCEDIETION 3 PACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBEIAI; COMPLEA (TPANSCPIPTION	REGULATION/DNA, DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN RETA 1: CHAIN: R:	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROJEIN BETA I; CHAIN: B;	DNA; CITAIN: L, E,				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;
SEQFOL D score																								
PMF			1.00				1.00							82.0								11.0-		
Verify score			0.68				0.72							0.02								0.08		
Psi Blast			5.1e-38		***		7.5e-34							1.2e-31								3.4e-29		
END			895				936							970								1005		
STAR T AA			748				611							780								847		
CHAI N ID			В				В							В								В		
PDB U			Іамс				lawc							lawc			en en					lawc		
SEQ ID NO:			1503				1503							1503								1503	-	_

PDB annotation	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIDERED PROTEIN
Coumpound	DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score							
PMF score		-0.11	86'0	1,00	66'0	0.76	1.00
Verify		0.05	0.26	0.60	0.37	0.07	0.64
Psi Blast		1.7e-29	3.4e-26	4.5e-32	1.1e-26	1.4e-24	7.5e-33
END		1045	862	937	898	862	941
STAR T AA	MT1	088	269	776	569	269	779
CHAI N ID		Ф			Ø	æ	e B
PDB ID		lawc	1648	15d8	1bix	1blx	1blx
SEQ ID NO:		1503	1503	1503	1503	1503	1503

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PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	INNAC; CELL CICLE INHIBITOR, PISINKAC, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN-2 DEPENDENT KINASE, HODMONE/GBOUTTH BACTOB	SIGNAT ING PROTEIN HET IX TITIBN	HELIX. ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC.	BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING	PROTEIN	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE	o inhibi i OK; Chain: A;			CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;			CVCT INL DEPENDENT KINA SE	4 INHIBITOR B: CHAIN: A:	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;	,			NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-
SEQFOL D score	,																			•					: ::			· ·	•
PMF score		0.84				0.99			0.77		1.00		0.65				1.00				,	<u>8</u>				,	0.31		
Verify score		0.42				0.39		•	0.23	}	0.81		-0.07				0.22					0.52					0.21		
Psi Blast		3.4e-31				6.8e-32			36-19		1.2e-32		1.4e-21				1.7e-30				,	6.8e-32					1.7e-31		
END AA		867		r - maion		894	,		833	}	606		881				998		- ·	_		894					812		
STAR T AA		697				748			693)	176		685				697				3	748					940		
CHAI N ID		₩				∢.			A	l !	A		Ą				∢	_		6		∢ _					Ω	_	
PDB ID		1bu9				1bu9			1d9s		1d9s		Ideq				lihb					qui					i i		
SEQ ID NO:		1503				1503			1503		1503		1503	-			1503	_				2021					1503		

_	-			T***								-											_				-,					
	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKBNFKB COMPLEY		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR.	IKBANFKB COMPLEX		COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANK YRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX
B-ALPHA; CHAIN: D:	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ţţ.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ŗ.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ů.	-	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B POU; CHAIN: B, D;
																•																
	1.00			1.00				9.				1.00				0.88					 8.			,		0.1				1	1.00	
	0.10			0.37				0.52				0.37				0.15		•			0.43					0.42				,	0.50	
	3e-34			3.4e-38				3e-41				3e-38				I.7e-31				,	7.5e-34					8.5e-38			•	,	36-35	
	912			823				947				983				812					25			· · •	000	788				300	787	
	693			722				747				176				640					693				,	17/					0//	
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	1503			1503			3	1503				1503				1503				2021	enci				1503	coci				1500	coci	
		912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT;	1ikn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D	1ikn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; F:KAPPA-B	Iika D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: CHAIN: C; F.KAPPA-B P50D SUBUNIT; CHAIN: C; F.KAPPA-B P65 SUBUNIT; Iika D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P65 SUBUNIT;	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P50D likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: D; CHAIN: A; NF-KAPPA-B P50D	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P50D likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: D; CHAIN: C; I-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; Iikn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P50D Iikn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P50D SUBUNIT; CHAIN: D; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; FXAPPA-B P50D SUBUNIT; CHAIN: C; FXAPPA-B P50D	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN; CHAIN; CHAIN; D; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN; D; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT;	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN; C; I-KAPPA-B P50D SUBUNIT; CHAIN; D; Ilikn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P50D CHAIN; A; NF-KAPPA-B P50D CHAIN; A; NF-KAPPA-B P50D CHAIN; A; NF-KAPPA-B P50D	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; LKAPPA-B P50D	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: CHAIN: CHAIN: C; L'KAPPA-B P6S SUBUNIT; CHAIN: C; L'KAPPA-B P6S SUBUNIT; CHAIN: C; L'KAPPA-B P6S SUBUNIT;	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT;	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT;	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; L-KAPPA-B P50D	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: D; CHAIN: J; CHAIN: C; I-KAPPA-B P50D SUBUNIT; CHAIN: J; CHAIN: D; CHAIN: J; CHAIN: D; CHAIN: J; CHAIN: D; CHAIN: J; CHAI	likn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 722 882 3.4e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 747 947 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-41 0.52 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; likn D 776 983 3e-38 0.37 1.00 NF-KAPPA-B P6S SUBUNIT; cHADNIT; CHAIN: C; LKAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; CHAIN: A; NF-KAPPA-B P6S SUBUNIT; likn B 400 812 1.7e-31 0.15 0.88 NF-KAPPA-B P6S CHAIN: C; LKAPPA-B P6S CHAPPA-B P6	11kn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT;	11kn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B PGS SUBUNIT; CHAIN: A; NF-KAPPA-B PS0D SUBUNIT; CHAIN: A; NF-KAPPA-B PS0D SUBUNIT; CHAIN: C; L-KAPPA-B PS0D SUBUNIT; CHAIN: C; L-KAPPA-B PS0D SUBUNIT; CHAIN: D; CHAIN: A; NF-KAPPA-B PS0D SUBUNIT; CHAIN: C; L-KAPPA-B PS0D SUBUNIT; CHAIN: C; L-KAPPA-B PS0D SUBUNIT; CHAIN: D; CHAIN: A; NF-KAPPA-B PS0D SUBUNIT; CHAIN: C; L-KAPPA-B PS0S CHAIN: B, D; L-KAPPA-B-ALPHA; CHAIN: B, D; L-KAPPA-B-B-ALPHA; CHAIN: B, D; L	11kn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B PGS SUBUNIT; CHAN: A; NF-KAPPA-B PS0D SUBUNIT; CHAN: A; NF-KAPPA-B PS0D SUBUNIT; CHAN: C; L-KAPPA-B PS0D SUBUNIT; CHAN: C; L-KA	likn D 693 912 3e-34 0.10 1.00 NF-KAPRA-B P6S SUBUNIT; CHAIN:	Ilkn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P6S SUBUNIT; CHAIN: A) NF-KAPPA-B P5D SUBUNIT; CHAIN: C; I-KAPPA-B P50D SUBUNIT; CHAIN: D; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P6S CHAIN: D; IIIII E 640 812 1.76-31 0.15 0.88 NF-KAPPA-B P6S; CHAIN: B, D; I-KAPPA-B P6S; CHAIN: B, C; I-KAPPA-B P6S; CHAIN: B, D; I-KAPPA-B P6S; CHAIN: B, C; I-KAPPA-	Ilikn D 693 912 34-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P65 SUBUNIT; CHAIN: C; I-KAPPA-B P65 CHAIN:	Iikn D 693 912 36-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT; CHAN: A; NF-KAPPA-B P50D SUBUNIT; CHAN: A; NF-KAPPA-B P50D SUBUNIT; CHAN: C; L-KAPPA-B P50D SUBUNIT; CHAN: C; L-KAPPA-B P50D SUBUNIT; CHAN: A; NF-KAPPA-B P50D SUBUNIT; CHAN: A; NF-KAPPA-B P50D SUBUNIT; CHAN: C; L-KAPPA-B P50D SUBUNIT; CHAN: A; NF-KAPPA-B P50D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: A; NF-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: A; NF-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: B; D; L-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: B; D; L-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: B; D; L-KAPPA-B P60D SUBUNIT; CHAN: C; L-KAPPA-B P60D SUBUNIT; CHAN: B; D; CHAN:	IIIRN D 693 912 3e-34 0.10 1.00 NF-KAPPA-B PGS SUBUNIT; CHANIC STAPPA-B PGS CHANIC STAPPA-B	IIIsn D 693 912 3e-34 0.10 1.00 NF-KAPPA-B P65 SUBUNIT;	IIIsr D 693 912 3e-34 0.10 1.00 NF-KAPPA-B-PGS SUBUNT; CHAIN: A; NF-KAPPA-B-PS0D SUBUNT; CHAIN: CHAIN: CHAIN: C; I-KAPPA-B-PS0D SUBUNT; CHAIN: C; I-KAPPA-B-PS0D SUBUNT; CHAIN: CHAIN: C; I-KAPPA-B-PS0D SUBUNT; CHAIN: B; I-KAPPA-B-PS0D SUBUNT; CHAIN: C; I-KAPPA-B-PS0D SUBUNT; CHAIN:	IIIGN D 693 912 3e-34 0.10 1.00 NF-KAPPA-B PGS UBUNIT: CHAIN: A: NF-KAPPA-B PSOD SUBUNIT: CHAIN: A: NF-KAPPA-B PSOD SUBUNIT: CHAIN: CHAIN: C: L-KAPPA-B PGS UBUNIT: C-HAIN:	IIIGN D 693 912 36-34 0.10 1.00 NF-KAPPA-B P6S UBUNIT; CHAIN: A, NF-KAPPA-B P80D SUBUNIT; CHAIN: C, I-KAPPA-B 190D SUBUNIT; CHAIN: C, I-KAPPA-B P6S UBUNIT; CHAIN: A, INF-KAPPA-B P6S UBUNIT; CHAIN: C, I-KAPPA-B P6S UBUNIT; C, I-KAPPA-B P6S UBUNI	III D 693 912 38-34 0.10 1.00 NF-KAPPA-B-PGS SIBUNIT: CAPPA-B-PGS SIBUNIT: C	IIIR D 693 912 38-34 0.10 1.00 N-KAPPA-B-RS SUBUNIT;	Itign D 693 912 3e-34 0.10 1.00 NF-KAPPA-B PSS SUBUNIT;

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PDB annotation	E, (TRANSCRIPTION REGULATION/ANK REBEAT); ANKYRIN 2 REPEAT HELIX	TRANSFERASE PARP-CF, DOLY(ADP-RIBOSE) TRANSFERASE, DOLY TO ANSTEED AST	GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE	-		GLYCOSYLTRANSFERASE, NAD(+)	 -		GABFBEIAI; COMPLEA (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	十			(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING.	2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	-		GABPBETAI; COMPLEX
Coumpound	I-KAPPA-B-ALPHA; CHAIN: E, F;	POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;		POLY (ADP-RIBOSE)	POLYMERASE; CHAIN: NULL;		GA BINDING PROTEIN ALPHA;	DECTEIN BETA 1. CHAPIL D.	DNA; CHAIN; D, E;				-	GA BINDING PROTEIN ALPHA;	PROTEIN BETA 1: CHANGE	DNA: CHAIN: D. E.					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B;
SEQFOL D score																							
PMF score		0.52		0.16			1.00							3: 3:							98.0		
Verify score		0.01		-0.24			0.46						000	0.22					•		0.15		_
Psi Blast		1e-35		1.7e-08			3,4e-35						30	6.8e-39							1.7e-36		
END		1128		1127	·		296						000	329							357		
STAR T AA		856		994			128						,	192 193							215		
CHAI N ID							m		-				f	מי							ф		
PDB ID		1a26		1a26			lawc		-		-		-	Iawc							lawc		
SEQ ID NO:		1504		1504			1504						3	1504		711					1504	-	

PDB annotation	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score					
PMF	•	1.00	1.00	1.00	0.95
Verify score		0.62	0.75	0.69	0.17
Psi Blast		36-43	1.5e-39	1.2e-33	1.2e-37
END		164	176	482	578
STAR T AA		23	26	335	402
CHAI N ID		m	В	Д	Ф
PDB CI		lawc	lawc	lawc	lawc
SEQ ID NO.		1504	1504	1504	1504

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PDB annotation	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATIONDNA) GABPALPHA; GABPBETA1; COMPLEX	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABFBE 1A1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYKIN KEPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(IKANSCKIPTION	REGULATION/DNA), DNA-BINDING,	ANKYRIN REPEATS	TRANSCRIPTIONSTRETOR
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;		GA BINDING PROTEIN AT PHA:	CHAIN: A; GA BINDING	FROIEIN BEIA I; CHAIN: B; DNA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA:	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;		-		GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;			
SEQFOL D score											105.28				-									
PMF		1.00			1 00	2												1.00						
Verify score		0.04			0.40) ;												0.47				•		
Psi Blast		3.4e-33			4 50.47	3					4.5e-47							8.5e-39						
END AA		119			644	;					644							640		•				
STAR T AA		437			401	<u> </u>					491						ı	496	· · · · · ·					- y y todakin
CHAI N ID		Д			ď	ı					æ							B						
PDB TD		lawc			Lavac						lawc							lawc					,	
SEQ ID NO:		1504			1504	5					1504							1504						

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PDB annotation	INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	TUMOR SUPPRESSOR TIJMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANK YRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,
Coumpound		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
SEQFOL D score	-										
PMF score		1.00	0.99	0.99	00'1	00'1	1.00	86.0	1.00	1,00	1.00
Verify		1.08	0.82	0.72	0.43	0.67	0.67	0.13	0.14	0.82	0.09
Psi Blast		3.4e-06	0.00014	4.5e-10	4.5e-36	36-39	Ie-28	3e-34	7.5e-39	1.5e-42	1.5e-41
END AA		941	935	933	317	164	483	581	614	643	701
STAR T AA		877	875	877	179	24	332	402	433	492	525
CHAI N ID		4	∢	∢	4						
PDB ID		150х	1b4f	lb4f	15d8	1648	1bd8	15d8	1bd8	1bd8	15d8
SEQ DO:	,	1504	1504	1504	1504	1504	1504	1504	1504	1504	1504

	PDB annotation	ANKYRIN MOTIF TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CERCENTIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN/ CYCLIN-DEPENDENT			
	Coumpound	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PISINK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
	SEQFOL D score									
	PMF score	1.00	0.94	1.00	1.00	66'0	0.53	06.1	0.01	1.00
r i frestrikation i jaar ja	Verify score	0.31	60.0	0.50	0.51	0.47	-0.32	0.45	-0.31	0.60
	Psi Blast	6e-41	4.5e-39	3e-41	1e-28	1.4e-28	1.2e-37	1.5e-35	1.2e-31	1.5e-39
	END	767	266	784	800	818	299	317	459	164
	STAR TAA	594	62	644	099	683	95	179	248	26
	CHAI			•				Ф	g.	മ
	FDB ED	1bd8	8Pq1	1bd8	1bd8	1bd8	15d8	lblx	1blx	1blx
	SEQ NO:	1504	1504	1504	1504	1504	1504	1504	1504	1504

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PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	COMPLEX (INHIBITOR	PROTEINKINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	AI DIA DETA CONTRU	ALFHA/BE1A, COMPLEA (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEINKINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BEIA, COMPLEX	COMMITTEE CONTINUES	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR
Coumpound		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; F19INK4D; CHAIN: B:	î		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	á			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	Ä				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	;á			CVCI IN DEBENIDENT KIND SE	6; CHAIN: A; P19INK4D; CHAIN:	B,		,	COLOR TO COMPANY TO STATE OF THE STATE OF TH	CYCLIN-DEPENDENT KINASE
SEQFOL D score																												
PMF score		1.00				0.99					1.00						1.00				-	1 00	3				90 1	1.00
Verify score		0.49				0.34					0.72						0.17					0.50					0.54	0.04
Psi Blast		4.5e-30		•		1.5e-41					7.5e-42						4.5e-45					00 10	Î				0 50 00	07-20
END		483				618					643						771					784	+				900	966
STAR T AA		332				435					464		-	***			594					548	5				660	200
CHAI N ID		В				B	. ***				В						<u>—</u>					ď	 a				٥	۵
PDB ID		1blx				1blx					iplx					1	1blx			-		514	VIO.				1115	IOIA
SEQ ID NO:		1504				1504					1504						1504					1504	5				1504	\$ 5

PDB annotation	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-
Соитроиид	6; CHAIN: A, P19INKAD; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE			
SEQFOL D score								
PMF score		0.99	0.92	1.09	1.00	1.00	1.00	1.00
Verify score		0.30	0.28	0.85	0.64	0.57	0.63	0.27
Psi Blast		1.4e-28	1.7e-36	1.26-35	1.4e-32	5.1e-33	6e-35	3e-35
END		81 80	334	176	640	802	617	164
STAR T AA		683	182	28	496	£99	485	49
CHAI N ID		В	Ą	¥	¥	¥	Ą	A
PDB ID		×Iq1	1bu9	1bu9	1bu9	ibu9	149s	s6p1
SEQ ID NO:		1504	1504	1504	1504	1504	1504	1504

PDB annotation	HELIX, ANKYRIN REPEAT	E SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	E SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT	E CELL CYCLE INHIBITOR P18-	INHIBITOR, PI8-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	+	NK4C(NK6); CELL CYCLE NHIBITOR, P18-NK4C(NK6).	ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	 -	INK4C(INK6); CELL CYCLE	INHIBITOR, PI8-INK4C(INK6),	NHIBITOR	 	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6 Difficult	TRANSCRIPTION FACTOR P65:						A- IKBANFKB COMPLEX	TRANSCRIPTION FACTOR P65;
Coumpound	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR CHAIN: A R.		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			NF-KAPPA-B P65 SUBUNIT:	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	NF-KAPPA-B P65 SUBUNIT;
SEQFOL D score															- 444	-								
PMF score		1.00	0.45	1.00		1.00	-	•••	1.00				1.00				0.00				0.30			1.00
Verify		0.32	0.17	0.40		0.84			99.0				0.47		•		-0.18				-0.38			0.36
Psi Blast		7.5e-38	6e-37	8.5e-36		1.2e-35			1.4e-32				1.7e-32				1.2e-35				1.7e-33			1.5e-48
END		643	770	333		176			640				108	ior io Vico			366				403			240
STAR T AA		517	585	182		28			496				663				156				210			28
CHAI N ID		₹	¥	V		₽			Ą				Ą				Δ				A			D
PDB CD		1d9s	1d9s	lihb		1ih			1ihb				lihb				lika				i i			Likn
SEO E	ğ	1504	1504	1504		1504			1504		-		1504				1504				15 2			1504

A	2					1		Commonman	
) K	TAA	*		score	score	D score		
								CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-AI PHA: CHAIN: D:	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
清	D	399	562	1.4e-30	-0.26	0.30		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
								CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; 1-KAPPA-	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
								B-ALPHA; CHAIN: D;	
lika Ek	А	525	715	5.1e-34	-0.26	90.0		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
								CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
						·		B-ALPHA; CHAIN: D;	
iżi.	Д	528	775	6e-60	-0.05	0.55		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
								CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
								SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
								B-ALPHA; CHAIN: D;	
<u>=</u>	Ω	558	748	1.7e-36	-0.36	0.25		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
								CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
								SUBUNIT; CHAIN: C; I-KAPPA-	IKBANFKB COMPLEX
								B-ALPHA; CHAIN: D;	
ik B	• Д	672	817	1.7e-36	0.20	0.92		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
								CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
							<u>.</u>	SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
								B-ALPHA; CHAIN: D;	
ij	А	8	296	8.5e-40	-0.05	0.80		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
	~							CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
								SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
								B-ALPHA; CHAIN: D;	
Likn	Δ	91	396	4.5e-40	-0.19	0.12		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
					m marin a			CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
								SUBUNIT; CHAIN: C; 1-KAPPA-	IKB/NFKB COMPLEX
								B-ALPHA; CHAIN: D;	
lm yo		213	317	3e-35	60.0	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
Imvo	-	365	482	6e-30	0.57	100		MYOTROPHIN: CHAIN: NITI.	ANK-REPEAT MYOTROPHIN

PDB annotation	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ACELYLATION, NMK, ANK-KEPEAL	ACETYLATION, MAR, ANK-REPEAT	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
Coumpound		MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	1 14 15 1 2 14 1 2 2 10 2 14 14 14 14 14 14 14 14 14 14 14 14 14	MYOTROPHIN; CHAIN: NULL	MYOTBOBHIN: CHAIN: NIII I	MIOINOFIEM, CHAIM: NOLL	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,			NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	Œ.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	Ť.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ú	,	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	Ť.
SEQFOL D score		,								-								710 100 ·	•		•										
PMF score		00'1	1.00	3	90.	98.0	0.00	0.58					0.93					0.36					0.96					0.41			
Verify score		0.51	0.03		99.0	0.57	70.0	-0.11					-0.17					-0.34					-0.01					0.08			10.7716
Psi Blast		36-39	1.5e-38	3	7.5e-39	6.80-25	0.00-23	6.8e-36					1.5e-40					1.2e-44					5.1e-33			-Ma P		1.5e-50			
END		644	165	3	794	799	122	366					424					458					£03					622	***		
STAR T AA		528	61		681	684	+ 60	154					154					208					209					365			
CHAI N ID								ы					ш					щ					ш					щ			
PDB ID		1myo	1myo		Imyo	1mvo	og mir	Infi					Infi					Infi	•				Infi		*****	•		Inf			-
SEQ NO:		1504	1504	,	1504	1504	toci	1504					1504					1504					1504					1504			

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PDB annotation	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK VR.N. 2 REPEAT HEL IX	COMPLEX (TRANSCRIPTION COMPLEX (TRANSCRIPTION (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRN 2 REPEAT HEI IX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELLX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRN 2 REPEAT HELLX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),
Coumpound	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;
SEQFOL D score			·	·			
PMF	0.95	1.00	0.99	1.00	0.49	1.00	0.98
Verify	0.08	0.35	0.34	-0.06	-0.13	0.22	0.12
Psi Blast	36-45	5.1e-37	1.7e-32	6e-57	1.3e-54	1.7e-36	6.8e-40
AA A	643	628	682	177	307	817	296
STAR T AA	429	463	490	528	19	672	88
CHAI NĐ	田	ъ	田	ជា	ជា	I	旦
PDB	Infi	ful	Infi	Infi	Infi	Jul	1nfi
SEQ ID NO:	1504	1504	1504	1504	1504	1504	1504

PDB annotation	ANKYRIN 2 REPEAT HELIX	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION,	EPH RECEPTORS, TYROSINE 2	PHOSPHORYLATION, SIGNAL	TRANSDUCTION, TYROSINE-	PROTEIN 3 KINASE	TYROSINE-PROTEIN KINASE NMR,	RECEPTOR OLIGOMERIZATION,	EPH RECEPTORS, TYROSINE 2	PHOSPHORYLATION, SIGNAL	TRANSDUCTION, TYROSINE-	PROTEIN 3 KINASE	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ANKYRIN REPEATS, CELL-CYCLE	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound		EPHRIN TYPE-B RECEPTOR 2; CHAIN; NULL;					EPHRIN TYPE-B RECEPTOR 2;	CHAIN: NULL;					REGULATORY PROTEIN SWI6;	CHAIN: A, B;		P53; CHAIN: A; 53BP2; CHAIN:	'n								P53; CHAIN: A; 53BP2; CHAIN:	'n.						
SEQFOL D score																																
PMF score		0.84					0.59						0.18			0.84									1.00							
Verify score		0.65					0.78						-0.22			-0.13		-							-0.03							
Psi Blast		0.00034					1.5e-09						6e-37			6e-30									4.5e-40				·		•	
END AA		935					933						784			695									722							
STAR T AA		875					877						527			366									528							
CHAI N ID													A			В							-	,	Д							
PDB ID		1sgg					lsgg						1sw6			1ycs						_			1ycs							
SEQ ID NO:		1504					1504						1504			1504									1504							

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PDB annotation	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION		SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	CHAPERONE HOP, TPR-DÖMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL
Coumpound	P53; CHAIN: A; 53BP2; CHAIN: B;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR I-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN:
SEQFOL D score			-				
PMF score	0.76	0.05	0.13	0.82	-0.03	0.31	-0.02
Verify	0.01	-0.10	-0.76	-0.25	0.02	0.05	0.00
Psi Blast	7.5e-39	1.7e-29	3e-14	6e-14	3.4e-14	6.8e-22	1.5e-11
END	254	190	262	262	161	161	110
STAR T AA	29	39	218	221	40	39	24
CHAI N ID	М				B	•	A
PDB ID	lycs	ial7	1bor	Ichc	1e96	lelr	1elw
SEQ ID NO:	1504	1507	1507	1507	1507	1507	1507

SEQ NO.	PDB UD	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
					·				C, D;	REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1507	1elw	¥	39	153	1.4e-21	0.13	0.24		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1507	1g25	4	221	262	4.5e-13	-0.20	0.37		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)
1507	Irmd		210	302	9e-17	0.13	0.84		RAGI; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1508	ladq,	•	352	531	8.5e-18	-0.07	0.64		IGG4 REA; CHAIN; A; RF-AN IGMLAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBICEMENTO INTIGE N) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGE N), RHEUMATOID FACTOR 2 AUTO- ANTIBODY COMPLEX
1508	1bih	A	262	628	5.1e-43	0.18	0.39		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	15ih	A	350	721	1.5e-43	0.34	0.49		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	पादा	А	449	812	1.7e-50	0.29	96.0		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bih	∢	450	813	1.7e-50			124.44	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,

PDB annotation	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HUMOFHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	T-CELL SURFACE GLYCOPROTEIN	IMMUNOGLOBULIN FOLD,	TRANSMEMBRANE,	GLYCOPROTEIN, T-CELL, 2 MHC,	LIPOPROTEIN, T-CELL SURFACE	GLYCOPROTEIN	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL	ADHESION	CELL ADHESION NEURAL CELL	AURESION CELT OFFT	ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL	ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL
Coumpound		HEMOLIN; CHAIN: A, B;			HEMOLIN; CHAIN: A, B;			HEMOLIN; CHAIN: A, B;			HEMOLIN; CHAIN: A, B;			T-CELL SURFACE	GLYCOPROTEIN CD4; CHAIN:	NULL		•		AXONIN-1; CHAIN: A;	AXONIN-1: CHAIN: A:		AXONIN-1; CHAIN: A;	A VONITAL 1. CHAIRL A.	AAOININ-1; CHAIN; A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;		AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;
SEQFOL D score																														
PMF		-0.07			0.36			0.49			0.21			0.42						0.53	0.41		0.62	100	۲.01	0.84	0.70		-0.08	-0.02
Verify score		0.00			0.15			90.0			81.0			0.42					•	-0.05	0.07		0.15	90.0	80.0	0.26	0.24		0.05	0.07
Psi Blast		5.1e-37	•	,	6.8e-40			4.5e-37			3.4e-46			1.5e-15						8.5e-49	1.5e-49		5.1e-63	10.44	++-a1	3.4e-55	5.1e-49		6.8e-37	7.5e-39
END · AA		335	•	3,	1073			447			1184			723						535	628		721	347	747	813	268		448	448
STAR T AA		4		ì	726			74			816			557						178	262		348	2	n	449	536		46	74
CHAI N ID		Ą			∢:			-₹			A .									¥	¥		Ą	\ <	¢	¥	¥		A	Ą
PDB 115		1bih		:	lbih	-		1bih			1bih			1cdy						1cs6	lcs6		10s6	1 Park	95	lcs6	1cs6	,	1cs6	Ics6
SEQ ID NO:		1508			1508			1508			1508			1508						1508	1508		1508	1500	9000	1508	1508		1508	1508

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PDB annotation	ADHESION 6	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	IKANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	CACTOR RECEPTOR	UNUW ITHER CHOIN UND WITH
Coumpound		AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR I; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	Ç	-	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	Ç, D; ·	FIREORI AST GROWTH	ווו איטיט וטהעלטאועון
SEQFOL D score												-												 ,/-								
PMF score		0.24	-0.01			-			-0.19					0.30						-0.15				-		0.21					0.54	177
Verify score		0.04	0.13						0.08					-0.16						0.23						0.17					-0.05	25.5
Psi Blast		8.5e-48	1.7e-38						5. ie-21					6.8e-21						3.4e-17						5.1e-23					8 50-38	20000
END		1185	1184			446		1	1260					346						146						535			,		809	3
STAR T AA		829	6001					,	10%					178						2						361					450	3
CHAI N ID		¥ •	ပ					,	ပ	,				C				•		၁				-		ပ					ر	,
PDB ID		1cs6	lcvs					,	Icvs					lcvs			******			Icvs						lcvs	-				leve	20121
SEQ US		1508	1508						1508			*=-:		1508	***************************************	*				1508						1508			,		1508	7,7

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PDB annotation	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH
Coumpound	FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
SEQFOL D score						
PMF score		0.27	0.21	-0.05	-0.15	0.06
Verify score		0.10	-0.42	0.07	0.05	0.23
Psi Blast		5.1e-24	8.5e-36	1.7e-24	1.7e-37	5.1e-34
END		260	812	896	966	1184
STAR T AA		19	642	737	813	1009
CHAI N ID		v	ပ	C	၁	Д
PDB ID		Icvs	levs	Icvs	lcvs	levs
SEQ NO:		1508	1508	1508	1508	1508

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PDB annotation	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL
Coumpound		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	Ω΄. Ω΄.		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	ຸດ ວ		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH
SEQFOL D score			-																									-				
PMF score		0.82				0.01						-0.05						0.25						0.71						0.30		
Verify score		-0.19				0.15						0.19						0.19				-		-0.02						0.13		
Psi Blast		1.2e-21	-		·	1.7e-33						6.8e-19						8.5e-25			_			3.46-35						1.2e-22		
END AA		346				447						146						535						628						260		
STAR T AA		178				27.1	_					2						361						450						19		
CHAI N ID		Q				Д						Ω						Д						Д						<u> </u>	•	
PDB ID		levs				levs						lcvs			•			lcvs						lcvs				·		lcvs		
SEQ ID NO:		1508				1508						1508						1508						1508						1508		

PDB annotation	TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	IKANSDUCIION, Z DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	VIRUS/VIRAL PROTEIN, RECEPTOR	CD155, PVR, HUMAN POLIOVIRUS,	ELECTRON MICROSCOPY, 2	POLIOVIRUS-RECEPTOR COMPLEX,	VIRUS/VIRAL PROTEIN, RECEPTOR	VIRUS/VIRAL PROTEIN, RECEPTOR	CD155, PVR, HUMAN POLIOVIRUS,
Coumpound	FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	, O, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	ີ່ ດີ ປ		POLIOVIRUS RECEPTOR;	CHAIN: R; VP1; CHAIN: 1; VP2;	CHAIN: 2; VP3; CHAIN: 3; VP4;	CHAIN: 4;		POLIOVIRUS RECEPTOR;	CHAIN: R; VP1; CHAIN: 1; VP2;
SEQFOL D score	,							•																ī	:		-			
PMF		0.00					0.04					-0.11					,	0.00						0.03					0.16	
Verify score		-0.31				, <u></u>	0.11					0.04						0.20						-0.35					-0.09	
Psi Blast		1.2e-36			****		1.7e-25					3,4e-34						3.4e-23						6e-22					1.3e-23	
END AA		812					968					966						1082						810					688	
STAR T AA		642					737					813						911						602					641	
CHAI N ID		Ω					Q					Ω						О					_	æ					ద	
FDB CD		lcvs					Icvs					lcvs						lcvs						1dgi					Idgi	
SEQ ID NO:		1508					1508					1508						1508						1508			**********		1508	

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PDB annotation	ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX,	VIRUS/VIRAL, PROTEIN, RECEPTOR CELL ADHESION NCAM; NCAM, IMMUNOGLOBUL DE CELD, CI VCOPROTEIN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GI YCOPROTEN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GI VCOPROTEN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GI YCOPROTEN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GI YCOPROTEN	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GI YCOPROTEIN	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;
Coumpound	CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;
SEQFOL D score											
PMF		0.00	0.30	0.42	0.22	0.92	0.07	0.99	0.01	0.75	0.24
Verify score		-0.36	0.02	0.11	90.0	0.34	0.23	0.02	0.16	0.25	-0.16
Psi Blast		3.4e-18	6.8e-17	5.1e-28	3.4e-17	3e-24	3.4e-25	1.7e-20	4.5e-22	6.8e-19	le-29
END		1184	346	433	517	645	722	798	997	982	447
STAR T AA		902	178	266	354	452	539	644	815	818	271
CHAI N ID		<u>لا</u>	Ą	• A	∢	4	A	A	A	¥	E
PDB ID		igb.	lepf	lepf	lepf	lepf]de]	lepf]dej	Jdə1	lev2
SEQ No:		1508	1508	1508	1508	1508	8051	1508	1508	1508	1508

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PDB annotation	IMMUNOGLOBUEN (20)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D, FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D, FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;
SEQFOL D score						
PMF score		0.04	0.07	-0.11	0.01	0.43
Verify score		0.10	-0.05	0.06	0.10	0.02
Psi Blast		5.1e-22	le-33	1.7e-31	5.1e-35	8.5e-21
END		535	628	966	1188	350
STAR T AA		361	454	825	1009	178
CHAI N ID	•	ក	ជា	m	Ð	g
PDB ID		1ev2	1ev2	1ev2	1ev2	lev2
SEQ ID NO:	71	1508	1508	1508	1508	1508

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PDB annotation	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS. B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOLL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS. B-FREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-
Coumpound	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: B, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN:
SEQFOL D score						
PMF score	-0.05	0.18	69'0	90.0	0.53	0.17
Verify score	0.0	0.13	0.41	-0.02	0.23	0.12
Psi Blast	8.5e-18	1.2e-32	6.8e-24	6.8e-34	1.7e-23	1.2e-21
END	152	451	538	628	724	264
STAR T AA		271	361	454		61
CEAI N ID		O	_ල	O	Ð	9
PDB ID	lev2	lev2	lev2	lev2	lev2	lev2
S e S	1508	1508	1508	1508	1508	1508

PCT/US02/05095

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
<u>eğ</u>	8	e N	TAA	Ψ¥		score	score	D score	-	
									E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	lev2	G	651	816	6.8e-34	-0.35	0.15		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
									FACTOR 2; CHAIN: A, B, C, D;	FACTOR RECEPTOR FGF2; FGFR2;
									FIBROBLAST GROWTH	IMMUNOGLOBULIN (IG)LIKE
									FACTOR RECEPTOR 2; CHAIN:	DOMAINS BELONGING TO THE I-
									E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE
_										DOMAINS, B-TREFOIL FOLD
1508	lev2	Ç	737	006	3.4e-25	0.08	0.23	1	FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
									FACTOR 2; CHAIN: A, B, C, D;	FACTOR RECEPTOR FGF2; FGFR2;
									FIBROBLAST GROWTH	IMMUNOGLOBULIN (IG)LIKE
	-,								FACTOR RECEPTOR 2; CHAIN:	DOMAINS BELONGING TO THE I-
									E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE
6/										DOMAINS, B-TREFOIL FOLD
1508	lev2	g	74	259	1.5e-22	0.18	0.51		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
		***************************************							FACTOR 2; CHAIN: A, B, C, D;	FACTOR RECEPTOR FGF2; FGFR2;
									FIBROBLAST GROWTH	IMMUNOGLOBULIN (1G)LIKE
									FACTOR RECEPTOR 2; CHAIN:	DOMAINS BELONGING TO THE I-
									E, F, G, H,	SET 2 SUBGROUP WITHIN IG-LIKE
										DOMAINS, B-TREFOIL FOLD
1508	lev2	ტ	825	1000	1.7e-33	0.04	-0.15		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
									FACTOR 2; CHAIN: A, B, C, D;	FACTOR RECEPTOR FGF2; FGFR2;
									FIBROBLAST GROWTH	IMMUNOGLOBULIN (IG)LIKE
									FACTOR RECEPTOR 2; CHAIN:	DOMAINS BELONGING TO THE I-
									E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE
										DOMAINS, B-TREFOIL FOLD
1508	lev2	G	911	1087	6.8e-22	0.02	-0.01		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
									FACTOR 2; CHAIN: A, B, C, D;	FACTOR RECEPTOR FGF2; FGFR2;
		-							FIBROBLAST GROWTH	IMMUNOGLOBULIN (IG)LIKE
									FACTOR RECEPTOR 2; CHAIN:	DOMAINS BELONGING TO THE 1-
									E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE
										DOMAINS, B-TREFOIL FOLD
1508	levi	ပ	178	346	5.1e-21	-0.26	0.33		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH
	-								FACTOR 1; CHAIN: A, B;	FACTOR RECEPTOREST FIGHRI;

PDB annotation	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD		GROWTH FACTOR/GROWTH FACTOR RECEPTOR EGEL-FOER1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
SEQFOL D score						
PMF score		-0.06	60:0-	0.18	0.19	0.04
Verify score		0.01	0.23	-0.15	-0.01	0.16
Psi Blast		8.5e-32	3.4e-19	3.4e-33	3e-16	1.2e-22
END		74	146	628	703	260
STAR T AA		27.1	72	450	552	61
CHAI N ID		ပ	U	O.	6 U	O .
PDB ID		levt	leví	levt	levt	levt
SEQ ID NO:		1508	1508	1508	1508	1508

PCT/US02/05095

PDB annotation	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEINFRESELTOR, ÍGE- BINDING 2 PROTEIN	MMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD,
	GRO FAC IMM DOM SET	GRO FAC IMM DOM SET DOM	ALPI GLY BINE	ALPI GLY BINE	MM ALPI GLY BINE	ALPI GLY BINE	ALPI GLY- BINE	ALPI
Coumpound	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON
SEQFOL D score								
PMF score	0.11	-0.03	0.06	0.48	0.92	0.63	0.17	0.12
Verify score	-0.32	0.05	0.14	0.32	0.26	-0.01	0.05	0.04
Psi Blast	1.4e-35	1.2e-24	1.5e-17	3e-21	1.5e-20	9e-18	1.7e-21	3e-19
END	812	968	538	153	539	727	795	900
STAR TAA	642	737	349	36	415	605	8	779
CHAI N ID	ပ	O	¥	₹	A	¥.	4	4
PDB ID	levt	levt	129	1f2q	12d	1129	1124	1f2q
SEQ NO.	1508	1508	1508	1508	1508	1508	1508	1508

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PDB annotation		GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN RECEIVER, TGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODI, IGE-FC	IMMONE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	GE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON)
Coumbound		RECEPTOR CHAIN: A;	HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; 1G	EPSILON CHAIN C REGION;	CHAIN: B, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; IG	EPSILON CHAIN CREGION;	CHAIN: B, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; 1G	EPSILON CHAIN C REGION;	CHAIN: B, D;		HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; 1G	EPSILON CHAIN C REGION;	CHAIN: B, D;	VTHATA USH	FIGH AFFINITI	IMMUNOCLUBULIN EFSILON	RECEPTOR CHAIN: A; IG	EFSILON CHAIN C REGION;	CHAIN: B, D;		HIGH AFFINITY IMMUNOGLOBULIN EPSILON
SEOFOL	D score																																
PMF	score		0.01						-0.02						0.30			•			0.24				*****	0.70	2.7						0.95
Verify	score		-0.01						60.0						0.16						0.35					10.01	0.21						0.37
Psi Blast			3.4e-19			M.dr			3.4e-17						6e-21						9e-20					750 10							7.5e-19
END	AA		430						538						152				,		538					317	240						726
STAR	T AA		258						346						39	-					415					151	1						566
CHAI	NB		Ą					•	٧						A			-			٧					-	<-						A
PDB	П		1f6a						1f6a						1f6a						1f6a					16%	1104						1f6a
SEO	Д ON ON		1508						1508						1508						1508					9051	9001						1508
_				_																													

PDB annotation	IGE-FC, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE-FC ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR,
Coumpound	RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;
SEQFOL D score							
PMF score		-0.11	0.11	0.10	0.65	0.55	0.86
Verify score		0.20	-0.14	0.27	0.11	0.38	0.28
Psi Blast		le-16	1.4e-20	1.5e-19	1.5e-15	1.2e-17	3e-19
END AA		751	795	006	666	534	148
STAR T AA		S	646	740	821	349	37
CHAI N ID		∢.	. ∢	₹	Ą	Ą	Ą
PDB ID		1f6a	1f6a	1f6a	1f6a	lfcg	1fcg
SEQ NO:		1508	1508	1508	1508	1508	1508

PDB annotation	IMMUNOGLOULIN, LEUKOCYTE, CD32	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN	
Coumpound		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	TELOKIN; CHAIN: A	TELOKIN; CHAIN: A	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	TLYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3
SEQFOL D score			3.						
PMF score		0.43	0.53	0.03	0.00	0.54	0.41	09:0	0.06
Verify		0.02	-0.26	0.20	-0.28	0.29	0.03	0.17	-0.34
Psi Blast		6e-19	6.8e-17	8.5e-16	8.5e-17	3e-18	3.4e-16	1.7e-15	61-99
END AA		645	766	1186	447	148	796	518	703
STAR T AA		456	820	1085	347	36	646	352	557
CBAI N ID		Ą	Ą	Ą	¥	¥	¥	<u></u>	Ą
PDB ID		1fcg	1fcg	1fhg	1fng	1fn1	1fhl	1gc1	Ihng
SEQ NO.		1508	1508	1508	1508	1508	1508	1508	1508

PCT/US02/05095

PDB annotation		COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	IMMUNOGLOBULIN IMMUNOGLOBULINGERYCE JONES PROTEIN		
Coumpound	T LYMPHOCYTE ADHESION GL YCOPROTEIN CD2 (RAT) IHNG 3	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	NTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	TWITCHIN; CHAIN; NULL;	LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	IMMUNOGLOBULIN
SEQFOL D score						* **.(*):	104.67	
PMF score	0.17	0.18	0.09	0.55	0.59	0.60		0.23
Verify score	90.0	-0.02	0.42	0.10	0.14	0.20		-0.05
Psi Blast	9e-15	1.5e-20	3e-20	1.7e-15	3.4e-14	8.5e-16	5.1e-17	1.5e-17
END	966	6.29	966	994	1185	531	543	884
STAR T AA	825	462	740	747	1084	355	143	538
CHAI N ID	4 '	В	æ	<u>a</u>		Ą	Ф	E
PDB ID	Ihng	Ħ.	litb	litb	1koa	III	, meo	Imco
SEQ ID NO:	1508	1508	1508	1508	1508	1508	1508	1508

PDB annotation		MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTEN; NEXTMS; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL
Coumpound	IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	TITIN; CHAIN; NULL;	TITIN: CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	P58-CL42 KIR; CHAIN: NULL;
SEQFOL D score			·			
PMF score		0.53	0.00	-0.12	0.04	-0.07
Verify score		0.58	-0.53	0.16	0.46	0.11
Psi Blast		1.7e-14	3.4e-11	5.1e-15	1.7e-13	3.4e-10
END		1185	762	449	721	149
STAR T AA		1086	178	349	643	526
CEAI N ID			_	•	,	
PDB ID		Inct	Inct	Inct	Inct	lnkr
SEQ ID NO:		1508	1508	1508	1508	1508

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PDBCHAISTARENDPsi BlastVerifyPMFIDN IDT AAAAAAscorescore	STAR END Psi Blast Verify TAA AA score	END Psi Blast Verify AA score	Psi Blast Verify score	ast Verify score	 PMF score	T .	SEQFOL D score	Conmpound	PDB annotation
									KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1nkr 813 995 1.7e-23 -0.01 0.13	995 1.7e-23 -0.01	995 1.7e-23 -0.01	1.7e-23 -0.01	-0.01	 0.13			P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1tm 1088 1185 1.7e-14 0.63 0.35	1185 1.7e-14 0.63	1185 1.7e-14 0.63	1.7e-14 0.63	4 0.63	0.35			MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
ltmm 178 262 3.4e-11 -0.22 0.00	262 3.4e-11 -0.22	262 3.4e-11 -0.22	3.4e-11 -0.22	-0.22	 0.00			MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
11mm 2 61 1.5e-09 0.30 -0.15	61 1.5e-09 0.30	61 1.5e-09 0.30	1.5e-09 0.30	0:30	 -0.15	<u></u>		MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1tmm 643 721 1.7e-13 0.50 0.04	721 1.7e-13 0.50	721 1.7e-13 0.50	1.7e-13 0.50	3 0.50	0.04			MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
lvca A 397 538 4.5e-15 -0.05 0.72	397 538 4.5e-15 -0.05	538 4.5e-15 -0.05	4.5e-15 -0.05	5 -0.05	 0.72			HUMAN VASCULAR CELL ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	CELL ADHESION PROTEIN VCAM- D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15
1vca A 557 680 4.5e-13 -0.15 0.00	557 680 4.5e-13 -0.15	680 4.5e-13 -0.15	4.5e-13 -0.15	3 -0.15	0.00	\perp		HUMAN VASCULAR CELL	CELL ADHESION PROTEIN VCAM-

								-														-		
PDB annotation		DI,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD.	TRANSMEMBRANE,	GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD,	TRANSMEMBRANE,	GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM	GLYCOPROTEIN CD4;	TRANSMEMBRANE.	GLYCOPROTEIN, T-CELL, 2 MHC	LIPOPROTEIN, POLYMORPHISM	CELL ADHESION ICAM-2; IMMI NOGI. OBLILIN FOLD, CELL	ADHESION, GLYCOPROTEIN, 2	TRANSMEMBRANE, REPEAT, SIGNAL	IMMUNE SYSTEM PS8 NATURAL	KILLER CELL RECEPTOR; KIR,	INHIBITORY RECEPTOR: 2	IMMUNOGLOBULIN	IMMUNE SYSTEM P58 NATURAL	KILLER CELL RECEPTOR; KIR,	NATURAL KILLER RECEPTOR,	INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM P58 NATURAL
Coumpound		ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	T-CELL SURFACE GLYCOPROTEIN CD4: CHAIN:	A, B;	-	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN:	A, B;	`	T-CELL SURFACE	A. B.			NTERCELLULAR ADHESION MOLECILE, 2: CHAIN: NIEL:			MHC CLASS I NK CELL	RECEPTOR PRECURSOR;			MHC CLASS I NK CELL	RECEPTOR PRECURSOR;	CHAIN: A;	f	MHC CLASS I NK CELL
SEQFOL D score	31036																							
PMF	3001		0.41		, .	0.13			89.0				0.05			-0.09				0.05				0.19
Verify	2020		0.09			-0.11			90.0				-0.09			0.19			-	0.28				0.00
Psi Blast			1.2e-26			6e-26			6e-23				1.5e-16			1.2e-19				4.5e-24				3e-16
END	§		703			882			1068				0001			534				643				723
STAR			364			552			740				22			347				451				536
CEAI		•	Ą	_		Ą			Ą							₹				Ą				4
PDB	1		1wio			1wio			1wio	-			Izxd			2dli				2dli				2dli
SEQ	S S S		1508			1508			1508				1508			1508			,	1508				1508

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PDB annotation	KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR,
Coumpound	RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;
SEQFOL D score					,							
PMF score		0.23	90:0-	-0.06	-0.02	0.27	0.75	0.65	0.65	0.47	0.00	-0.05
Verify score		0.20	0.22	0.17	0.01	0.25	0.28	-0.04	0.19	0.38	0.04	0.08
Psi Blast		3e-21	1.2e-09	5.1e-22	7.5e-15	3.4e-18	7.5e-21	3e-20	1.2e-16	3e-20	3.4e-17	4.5e-19
END AA		256	148	991	349	537	151	536	724	868	666	866
STAR T AA		19	7	813	152	349	37	415	528	740	820	825
CHAI N ID		₹	¥	¥	4	¥	¥	¥	₹	Ą	Ą	Ą
PDB ID		2dli	2dli	2dli	2fcb	2fcb						
SEQ ID NO:		1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508

PDB annotation	FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	CELL ADHESION PROTEIN NCAM MODULE 2: CELL ADHESION,	GLYCOPROTEIN, HEPARIN-	ADHESION MOLECULE,	IMMUNOGLOBULIN FOLD, HOMOPHILC 3 BINDING, CELL.	ADHESION PROTEIN			HYDROLASE PNB ESTERASE;	ALPHA-BETA HYDROLASE,	ACTIVITY, 2 PNB ESTERASE	CHOLINESTERASE SERINE	HYDROLASE,	NEUROTRANSMITTER CLEAVAGE,	CATALYTIC 2 TRIAD, ALPHA/BETA HYDROL ASE	HYDROLASE MACHE; HYDROLASE,	SERINE ESTERASE,	ACETYLCHOLINESTERASE,	TETRAMER, 2 HYDROLASE FOLD,	GLYCOSYLATED PROTEIN	HYDROLASE BILE SALT	ACTIVATED LIPASE BILE SALT	ESTERASE, LIPASE
Coumpound		FC GAMMA RIIB; CHAIN: A;	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM:	CHAIN: A;	-			IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN	IMMUNOGLOBULIN IGGI	PARA-NITROBENZYL	ESTERASE; CHAIN: A;		ACETYLCHOLINESTERASE;	CHAIN: A;			ACETYLCHOLINESTERASE;	CHAIN: A, B, C, D;	المود			CHOLESTEROL ESTERASE;	CHAIN: NULL;	
SEQFOL D score																								
PMF score		0.70	0.12					0.47		0.22			0.12			-	0.43					90.0		
Verify score		0.00	0.42					0.05		-0.24			-0.23				-0.29			,		-0.50		
Psi Blast		3e-18	1.7e-12					5.1e-18		9e-13			16-21				5.1e-22	٠				3.4e-19	· No.	
END AA		9801	722		-			529		64			73				73					74	-2-0	
STAR T AA		216	642					353		4			3				3					<u>س</u>		
CHAI		¥	<					¥		4			¥				Ą							
PDB ID		2fcb	3ncm					8fab		Ic7j			lea5			and the second	1maa					2bce		
SEQ ID NO:		1508	1508					1508	,	1510			1510				1510					1510		

CHAI STAR END NID TAA AA G 241 274	STAR END Psi Blast Verify StD TAA AA Score Score StD StD	AA Score score 274 3 42-08 0 14 -	Psi Blast Verify score	st Verify score	gg g	Sco.	E 2	SEQFOL D score	Coumpound DNA: CHAIN: A B D E:	PDB annotation COMPLEX (ZINC FINGER/DNA) ZINC
241 274 3.46-08 0.14.	241 274 3.46-08 0.14.	274 3.46-08 0.14.	3.46-08 0.14.	0.14		-0.11			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEA (AINC FINGERODA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
2adr 1 39 5.1e-11 -0.78 0.03	5.1e-11 -0.78	5.1e-11 -0.78	5.1e-11 -0.78	-0.78	W	0.03		·	ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
2adr 403 446 1.7e-11 0.09 -0.20	446 1.7e-11 0.09	446 1.7e-11 0.09	1.7e-11 0.09	0.09		-0.2	0		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR I, ZINC FINGER, NMR
2pro A 81 166 4.5e-10 0.03 -0.19	81 166 4.5e-10 0.03	166 4.5e-10 0.03	4.5e-10 0.03	0.03		<u>-</u>	6		ALPHA-LYTIC PROTEASE; CHAIN: A, B, C;	PRO REGION PRO REGION, FOLDASE, PROTEIN FOLDING, SERINE PROTEASE
lez3 A 432 543 4.5e-09 -0.01 0.09	432 543 4.5e-09 -0.01	543 4.5e-09 -0.01	4.5e-09 -0.01	-0.01		0.0			SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
200	164 500 5.1e-25 0.21	500 5.1e-25 0.21	5.1e-25 0.21	5 0.21		1.00			RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITORANDCLEASE) COMPLEX (INHIBITORANDCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1a4y A 243 469 3e-34 0.34 1.00	243 469 3e-34 0.34	469 36-34 0.34	36-34 0.34	0.34	<u> </u>	1.00			RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS

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PDB annotation	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-
Coumpound	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB			
SEQFOL D score			113.01				
PIMF score	8.1	0.95		0.90	0.48	0.39	0.19
Verify score	0.51	0.05		-0.03	-0.27	-0.30	0.07
Psi Blast	3e-35	3.4e-24	6.8e-32	6.8e-32	1.2e-23	1.7e-21	1.7e-10
END	469	407	496	471	438	495	474
STAR T AA	282	7	2	98	267	316	350
CHAI N ID	∢	¥	. •	Y	¥	Ą	Ą
PDB ID	184y	la4y	1a4y	1a 4 y	140b	1405	Idce
SEQ ID NO:	1521	1521	1521	1521	1521	1521	1521

SPQ PDB CRAI STAR END Fel Blast Verify PMI SEQPOL Commpound FDB annotation NOD ID ND T AA AA 401 471 1.5e-66 -0.04 0.39 NUCLEAR RAN EXPORT RNA BINDING PROTEIN TAP (NFX). 1521 Ifol A 401 471 1.5e-66 -0.04 0.39 NUCLEAR RAN EXPORT RNA BINDING PROTEIN TAP (NFX). 1521 Ifol A 401 471 1.5e-66 -0.04 0.39 NUCLEAR RAN EXPORT RNA BINDING PROTEIN TAP (NFX). 1521 Ifol A 401 471 1.5e-66 -0.04 0.39 NUCLEAR RAN EXPORT RNA BINDING PROTEIN TAP (NFX). 1521 Ifp A 254 512 1.7e-12 -0.00 0.03 SCPCTAN. C.CALIN. A.B. RRAN BINDING PROTEIN TAP (NFX). 1521 Ifp A 254 512 1.7e-12 -0.00 0.03 SCPCTAN. C.CALIN. A.CCTOR I.CALIN. A.B.		·	·	,				,
PDB CHAI STAR END Psi Blast Verify PMF SEQFOL	PDB annotation	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	RNA BINDING PROTEIN TAP (NFXI), RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LHDORESPECHE REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIOUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION RNA 1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNA 1P, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRY	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN
PDB CHAI STAR END Psi Blast Verify PMF	Coumpound	GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, I, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO;
PDB CHAI STAR END Psi Blast Verify Store	SEQFOL D score					•	1949 1948 (Alexander) 1944 (Alexander)	
PDB CHAI STAR END Psi Blast STAR ST	PMF		0.39	0.28	0.03	0.51	\$.	86.0
PDB CHAI STAR END Psi	Verify score		-0.04	-0.07	-0.00	0.08	80.0-	0.17
PDB CHAI STAR			1.5e-06	1.5e-06	1.7e-12	8.5e-13	67-88-9	5.1e-21
2 PDB CHAI 1501 A 1501 B 1502 A 1572 A	END AA		471	471	512	514	8 8	474
2 PDB	STAR T AA		401	401	254	323	157	215
	CHAI N ID		A	B	A	¥	Ą	Ą
SEQ DB NO: 1521 1521 1521 1521 1521 1521 1521 152	PDB		1601	lfol	1fqv	1152	1yrg	lyrg
	SEQ No.		1521	1521	1521	1521	1521	1521

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PDB annotation	FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE. 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRY	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRY	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	
Coumpound	CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	
SEQFOL D score				109.97		
PMF score		0.55	0.28		0.81	
Verify		E: 0	0.10		0.12	
Psi Blast		4.5e-30	3.4e-09	8.5e-46	8.5e-46	
END		469	508	491	511	
STAR T AA		243	348	42	68	
CHAI N ID	The state of the s	¥	4			
PDB ID		lyrs	lyrg	2bnh	2bnh	
SEQ ID NO:		1521	1521	1521	1521	

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PDB annotation	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE		LIGASE CYCLIN A/CDK2-	A/CDK2-ASSOCIATED PROTEIN P19;	SKP1, SKP2, F-BOX, LRR, LEUCINE-	RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE SKP2 F-BOX; SKP1; SKP1,	SKP2, F-BOX, LRR, LEUCINE-RICH	REPEAT, SCF, UBIQUITIN, 2 E3, I IBIOI IIIN PROTEIN 1 164 SE	LIGASE CYCLIN A/CDK2-	ASSOCIATED P45; CYCLIN A/CDK2-	ASSOCIATED P19; SKP1, SKP2, F-	BOX, LRRS, LEUCINE-RICH	REPEATS, SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION TUMOR	SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2
Coumpound	TROPOMYOSIN; CHAIN: A, B, C, D	COLICIN IA; CHAIN: NULL;	SYNTAXIN-1A; CHAIN: A, B, C;	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;		SKP2; CHAIN: A, C, E, G, I, K, M, O. SKP1; CHAIN: B, B, B, H, T, T	N, P;		1	CYCLIN A/CDK2-ASSOCIATED	P19; CHAIN: A, C; CYCLIN	A/CDK2-ASSOCIATED P45; CHAIN: B. D:	SKP2; CHAIN: A, C; SKP1;	CHAIN: B, D;					ELONGIN B; CHAIN: A, D, G, J;	ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;
SEQFOL D score			-				-										•			
PMF score	-0.20	-0.20	-0.14	-0.20		1.00				0.62			0.99						9.	
Verify score	0.46	0.36	0.36	0.11		0.78				0.21	-		0.48						0.76	·
Psi Blast	4.5e-08	1,5e-08	1.1e-12	4.5e-08		1.7e-24				1.7e-24			1.7e-24						3.4e-16	
END	142	142	143	142		22				82			82						0%	
STAR T AA	54	20	20	20						<u> </u>		-	17]	17	
CHAI N ID	A	·	Ą	А		<u> </u>				മ			33						20	
PDB CC	lc1g	lcii	Jez3	1raq	7	Ifqv				Igi			1fs2	*****		-		ļ.	1vcb	
SEQ No.	1522	1522	1522	1522		1523				1523			1523						1523	

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PDB annotation	TRANSCRIPTION, TRANSCRIPTION	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE,	TPASE ACTIVATING PROTEIN, GAP,	CDC42, 2 PHOSPHOINOSITIDE 3-	NINASE, SHS DOMAIN, SHZ DOMAIN, 3 SIGNAL	TRANSDUCTION	PHOSPHOIKANSFERASE KHOGAP	TPASE ACTIVATING PROTEIN GAD	CDC42, 2 PHOSPHOINOSITIDE 3-	KINASE, SH3 DOMAIN, SH2	DOMAIN, 3 SIGNAL	TRANSDUCTION	PHOSPHOTRANSFERASE RHOGAP	DOMAIN; PHOSPHOTRANSFERASE,	TPASE ACTIVATING PROTEIN, GAP,	CDC42, 2 PHOSPHOINOSITIDE 3-	KINASE, SH3 DOMAIN, SH2	DOMAIN, 3 SIGNAL	TRANSDUCTION	PHOSPHOTRANSFERASE RHOGAP	DOMAIN; PHOSPHOTRANSFERASE,	TPASE ACTIVATING PROTEIN, GAP,	CDC42, 2 PHOSPHOINOSITIDE 3.	KINASE, SH3 DOMAIN, SH2
Coumpound		ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;		•		MICONIA TERMINA	FRUSERALIDITANOSITOL 3-	MINASE; CHAIN: A, B;					PHOSPHATIDYLINOSITOL 3-	KINASE; CHAIN: A, B;				-		PHOSPHATIDYLINOSITOL 3-	KINASE, CHAIN: A, B;			-
SEQFOL D score		52.02												67.87		•						*****			
PMF score			0.63				001	3													0.76				
Verify score			0.10				53.0	}													0.09				
Psi Blast		3.4e-16	6.8e-19			-	150.35	2						3e-36							6.8e-19				
END AA		84	291				304	{						312						-	291				
STAR T AA		17	122				125	}					1	107					•		122				
CHAI N ID		щ	∢				A	!					,	2 0							— Ф				
PDB ID		lvcb	Ipbw		~~~	,aea	1nhw						 - -	Modi		•				╅	Mqd1				
SEQ ID NO:		1523	1524				1524						, 6, ,	1224							1524				

4.70.946+1.40₁.769+1

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DOMAIN, 3 SIGNAL TRANSDUCTION	PHOSPHOTRANSFERASE RHOGAP	DOMAIN; PHOSPHOTRANSFERASE,	TPASE ACTIVATING PROTEIN, GAP,	CDC42, 2 PHOSPHOINOSITIDE 3-	KINASE, SH3 DOMAIN, SH2	DOMAIN, 3 SIGNAL	TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	GAP, SIGNAL-TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	GAP, SIGNAL-TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN,	GAP, SIGNAL-TRANSDUCTION	COMPLEX(GTPASE	ACTIVATN/PROTOGENEOUGENE)	GTPASE-ACTIVATING PROTEIN	RHOGAP; COMPLEX (GTPASE	ACTIVATION/PROTO-ONCOGENE),	GTPASE, 2 TRANSITION STATE, GAP	COMPLEX(GTPASE	ACTIVATN/PROTO-ONCOGENE)	GTPASE-ACTIVATING PROTEIN	RHOGAP; COMPLEX (GTPASE	ACTIVATION/PROTO-ONCOGENE),	GTPASE, 2 TRANSITION STATE, GAP	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)	GTPASE-ACTIVATING PROTEIN	RHOGAP: COMPLEX (GTPASE
	PHOSPHATIDYLINOSITOL 3-	KINASE; CHAIN: A, B;						RHOGAP; CHAIN: NULL;			RHOGAP; CHAIN: NULL;		,	RHOGAP; CHAIN: NULL;			P50-RHOGAP; CHAIN: A;	TRANSFORMING PROTEIN	RHOA; CHAIN: B;		-		P50-RHOGAP; CHAIN: A;	TRANSFORMING PROTEIN	RHOA; CHAIN: B;				P50-RHOGAP; CHAIN; A; TRANSFORMING PROTEIN	RHOA; CHAIN: B;	
						:								97.96															107.06		
	0.95							1.00		-	0.54						1:00						1.8 8								
	0.44							0.77			0.08						0.88		•				0.18								
	36-36							1.5e-37			1e-29			1.5e-37			7.5e-39						1.7e-29						7.5e-39		
	311			,				308			277			308			308					,	304						308		
	125							112			00			00 00			112						2						16		
	Д					•											₽.			•	• • •	-	<						<		
	Ipbw						1	17gg	•		Irgp		1	<u> </u>		,	4X		******			+							17X4		
	1524							1524			1524			1524			1524						1524						1524		
		125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3-	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B; 1/EP 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B; 1rgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B; 1rgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B; Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B; Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- Ingp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; 1rgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; 1rgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- Ingp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; 1rgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; 1rgp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL;	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3. Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; 6 Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; 6 Irgp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL; 6	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3. Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; 6 Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; 6 Irgp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL; 6	IPEP 125 311 36-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B; 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; 112p 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; 112p 88 308 1.5e-37 1.00 P50-RHOGAP; CHAIN: NULL; 112p 112 308 7.5e-39 0.88 1.00 P50-RHOGAP; CHAIN: A; 112p 12p 12p	ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; Irgp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL; Irgp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL; Irgp A 112 308 7.5e-39 0.88 1.00 P50-RHOGAP; CHAIN: A;	1pbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- FINESPECHAIN: A, B; FINESPECHAIN: A, B; FINESPECHAIN: A, B; FINESPECHAIN: NULL; FINESPECHAIN: NULL; FINESPECHAIN: NULL; FINESPECHAIN: NULL; FINESPECHAIN: NULL; FINESPECHAIN: NULL; FINESPECHAIN: A; FINESPECHAIN: A; FINESPECHAIN: A; FINESPECHAIN: B; FINESPECHA	1pbw B 125 311 36-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- FIND FINASE; CHAIN: A, B; FINE 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; FINE 112 308 1.5e-37 0.08 0.54 RHOGAP; CHAIN: NULL; FINE 112 308 1.5e-37 57.96 RHOGAP; CHAIN: NULL; FINE 112 308 7.5e-39 0.88 1.00 P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN 112 308 7.5e-39 0.88 1.00 RHOA; CHAIN: B; 1.00	Ipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- FINASE; CHAIN: A, B; FINASE; CHAIN: NULL; FINASE FINASE; CHAIN: NULL; FINASE FINAS	1pbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; CHAIN: B; CHAIN: CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: B; CHAIN: CHA	1pbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- FINANSE, CHAIN: A, B; 112 308 1.5e-37 0.77 1.00 RHOGAP, CHAIN: NULL; 11gp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; 11gp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL; 11gh 112 308 7.5e-39 0.88 1.00 P50-RHOGAP; CHAIN: A; 112 304 1.7e-29 0.18 1.00 P50-RHOGAP; CHAIN: B; 11gh 11g	lipbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- Irgp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NULL; Irgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NULL; Irgp 88 308 1.5e-37 97.96 RHOGAP; CHAIN: NULL; Ib4 A 112 308 7.5e-39 0.88 1.00 RHOGAP; CHAIN: NULL; Ib4 A 112 308 7.5e-39 0.88 1.00 RHOGAP; CHAIN: A; Ib4 A 112 304 1.7e-29 0.18 1.00 PSO-RHOGAP; CHAIN: B; Ib4 A 91 304 1.7e-29 0.18 1.00 PSO-RHOGAP; CHAIN: A; 0	1pbw B 125 311 36-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- 1	1pbw B 125 311 36-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE, CHAIN: A, B;	1pbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B; 11gp 112 308 1.5e-37 0.77 1.00 RHOGAP; CHAIN: NUIL; 1rgp 88 277 1e-29 0.08 0.54 RHOGAP; CHAIN: NUIL; 1pd A 112 308 7.5e-39 0.88 1.00 P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN 1bd A 91 304 1.7e-29 0.18 1.00 P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN 1bd A 91 304 1.7e-29 0.18 1.00 RHOA; CHAIN: B; 1.00 TRANSFORMING PROTEIN 1.00 TRANSFOR	1pbw B 125 311 3e-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B; Constant of the constant of th	11pbw B 125 311 36-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3. KINASE; CHAIN: A, B; 11gp 112 308 1.56-37 0.77 1.00 RHOGAP; CHAIN: NULL; 11gp 88 277 16-29 0.08 0.54 RHOGAP; CHAIN: NULL; 11pq 88 308 1.36-37 97.96 RHOGAP; CHAIN: NULL; 11pq 88 308 1.36-39 0.88 1.00 F50-RHOGAP; CHAIN: NULL; 11pq RHOGAP; CHAIN: NULL; 11pq RHOGAP; CHAIN: NULL; 11pq RHOGAP; CHAIN: NULL; 11pq RHOGAP; CHAIN: B; 11pq 1pq 1pq	1ppw B 125 311 36-36 0.44 0.95 PHOSPHATIDYLINOSITOL 3- Ingp 112 308 1.56-37 0.77 1.00 RHOGAP; CHAIN: NULL; 1rgp 88 277 16-29 0.08 0.54 RHOGAP; CHAIN: NULL; 1rgp 88 308 1.56-37 0.78 0.08 0.54 RHOGAP; CHAIN: NULL; 1rgp 112 308 7.56-39 0.88 1.00 P50-RHOGAP; CHAIN: NULL; 1rgh 4 112 304 1.76-29 0.18 1.00 P50-RHOGAP; CHAIN: B; 1.00 RHOA; CHAIN: B; 1.00 RAOA; CHAIN: B; 1.00 R

PDB annotation	ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME	LIGASE UBIQUITIN, UBIQUITIN. CONJUGATING ENZYME, YEAST	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN- CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN- CONJUGATING ENZYME; UBIQUITIN-CONJUGATING
Coumpound		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBC9; CHAIN: NULL;	UBC9; CHAIN: NULL;
SEQFOL D score		92.22		·	80.53		106.20	HERAL F	73.11
PMF score			00.1	66.0		1.00		1.00	
Verify score			19'0	0.36		0.57		0.83	
Psi Blast		1e-40	1e-40	8.5e-33	8.5e-33	3.4e-51	3.4e-51	3.46-38	3.4e-38
END		134	128	129	129	130	131	130	131
STAR T AA		-	4	5	ري د	1	4	·	
CHAI N ID	-	A	₹.	Q	۵	Ą	Ą	⊀	4
PDB ID		layz	layz	1c4z	1042	lgcq	1qcq	1u9a	lu9a
SEQ NO.		1525	1525	1525	1525	1525	1525	1525	1525

PDB annotation		ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE	UBIQUITIN CONJUGATION UBCI; UBIOUITIN CONJUGATION, LIGASE	UBIQUITIN CONJUGATION UBCI; UBIOUTIN CONJUGATION, LIGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOFSTER 2 ROND I IGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	UBIQUITIN CONJUGATION UBC7; -UBIQUITIN CONJUGATION, LIGASE, YEAST	COMPLEX (INHIBITORNUCLEASE) COMPLEX (INHIBITORNUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, BPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
Coumpound			UBIQUITIN CONJUGATING ENZYME: CHAIN: NULL:	UBIQUITIN CONJUGATING ENZYME: CHAIN: NULL:	UBIQUITIN CONTUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONIUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONIUGATING ENZYME; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
SEQFOL D score			96.00		82.57		77.96			67.17
PMF score				1.00		1.00		1.00	0.03	
Verify				0.49		99.0		0.80	-0.14	
Psi Blast			1.2e-41	1.2e-41	1.5e-37	1.5e-37	1.7e-36	1,7e-36	5.1e-19	3.4e-18
END AA			126	127	132	124	132	128	338	473
STAR T AA			-		-	(n	7	m	10	10
CHAI N ID		•					·		∀	¥
PDB U			2aak	2aak	2620	2e2c	2ucz	Zucz	1a4y	1a4y
SEQ	SO.		1525	1525	1525	1525	1525	1525	1527	1527

PDB annotation	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPPATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP-RIBONI/CLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIRONI ICT EOPPOTEIN	COMPLEX (NUCLEAR PROTEIN PROTEIN/NO) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONICI FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
Coumpound	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score			·				
PMF score	0.68	0.76	0.99	09.0	0.01	0.22	0.13
Verify	0.07	0.27	0.36	0.50	0.25	0.36	0.18
Psi Blast	9e-28	3.4e-18	1.5e-34	3e-25	7.5e-24	1.5e-14	3.4e-07
END AA	335	415	309	284	291	326	339
STAR T AA	134	25	99	140	164	212	232
CHAI N ID	Ą	A	A	¥	¥	Ą	¥
PDB ID	la4y	1a4y	1a4y	1a9n	1a9n	la9n	la9n
SEQ ID NO:	1527	1527	1527	1527	1527	1527	1527

PDB annotation	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP RIBONI (CL. EOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN'RNA) COMPLEX (NUCLEAR PROTEIN'RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCI, EOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP RIBONICI FOPROTFIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIRONI ICI HOMBOTTI	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX
Coumpound	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN; A, C; U2 B"; CHAIN; B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B", CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A; CHAIN; A, C; U2 B"; CHAIN; B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A'; CHAIN: A, C; U2 B";
SEQFOL D score									
PMF	0.68	0.98	0.43	0,45	0.27	0.00	0.43	0.96	0.70
Verify score	0.42	0.15	0.23	0.25	0.37	0.03	0.36	0.37	0.16
Psi Blast	1.7e-07	1.5e-24	3e-26	4.5e-26	9e-15	3.4e-05	1.7e-07	3e-24	1e-24
END	146	187	234	290	326	56	146	187	215
STAR T AA	43	51	26	140	212	23	43	51	89
CHAI N ID	٧	4	Ą	၁	၁	၁	c	ບ	•
PDB ID	la9n	la9n	la9n	129n	la9n	la9n	la9n	la9n	1a9n
SEQ ID NO:	1527	1527	1527	1527	1527	1527	1527	1527	1527

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PDB annotation	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONI (CI. EOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA,	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHI AMYDOMONAS, RI AGRITA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHIANYDOMONAS, ELACELLA	CONTRACTUE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
Coumpound	CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;
SEQFOL D score							,		
PMF score		0.69	0.99	0.10	0.70	0.15	9.06	-0.09	0.23
Verify score		0.43	0.35	-0.07	0.12	0.31	-0.40	0.12	-0.08
Psi Blast		3e-26	8.5e-24	3,4e-18	3.4e-23	1.2e-10	1.5e-18	5.1e-15	16-09
END AA		234	311	377	188	121	291	338	145
STAR T AA		92	129	228	4	21	167	217	43
CHAI N ID		O	A	¥	∀	₹ .	٠	¥	∢
PDB ID		la9n	140b	1406	1d0b	Idce	Jds9	1489	lds9
SEQ ID NO:		1527	1527	1527	1527	1527	1527	1527	1527

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PDB апвоtation	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN ACENCE ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIOUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP,
Coumpound	OUTER ARM DYNEIN; CHAIN: A;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;
SEQFOL D score							
PMF	0.15	0.01	0:30	0.36	-0.03	0.04	-0.03
Verify	-0.39	-0.15	0.16	-0.05	0.21	0.00	0.16
Psi Blast	1.4e-11	3.4e-07	3.4e-07	1.5e-15	1.3e-20	5.1e-12	6.8e-12
END AA	235	308	308	347	334	311	360
STAR T AA	73	227	227	134	125	171	62
CHAI N ID	¥	Ą	В	• •	. ⊀	¥	4
PDB ID	9sp1	1691	1f01	1fqv	1fs2	1£s2	Гутв
SEQ ID NO:	1527	1527	1527	1527	1527	1527	1527

PDB annotation	LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRY	TRANSCRIPTION RNA IP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA IP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X- RAY 2 STRUCTURE, APLYSIA KV1.1	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT	SIGNALING PROTEIN VOLTAGE-
Coumpound		GTPASE-ACTIVATING PROTBIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	KV1.2 VOLTAGE-GATED
SEQFOL D score		;						
PMF score		0.15	0.74	18.0	0.86	0.28	0.41	0.43
Verify score		0.11	0.08	0.01	0.66	60'0	0.48	0.48
Psi Blast		16-30	1.2e-22	1.26-40	1.5e-13	7.5e-12	1.2e-11	3e-12
END		265	413	312	207	204	210	208
STAR T AA		98	25	64	117	117	211	117
CHAI N ID		₽ ¥				Ą	ਤ	Ą
PDB ID		l yrg	2bnh	2bnh	1268	.1dsx	lexb	Iqdv
SEQ ID NO:		1527	1527	1527	1528	1528	1528	1528

printers -	-				 												
PDB annotation		GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KVI.1, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE	NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR	GTP BINDING PROTEIN HEADER TER	GUANINE NUCLEOTIDE EXCHANGE	NUCLEOTIDE EXCHANGE FACTOR,	GEF, RAN, 2 RAS-LIKE NUCLEAR	GIP BINDING PROTEIN HEADER TER	GUANINE NUCLEOTIDE EXCHANGE	FACTOR RCC1; GUANINE	NUCLEOTIDE EXCHANGE FACTOR, GRE RAN 2 RAS. I IKE NIICI FAR	GTP BINDING PROTEIN HEADER	TER	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE
Coumpound	i	POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KVI.1; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	REGULATOR OF CHROMOSOME	CONDENSATION I; CHAIN: A, B, C;		REGULATOR OF	CONDENSATION 1; CHAIN: A,	В, С;		REGULATOR OF	CHROMOSOME	CONDENSALION I; CHAIN: A, B. C:			HUMAN SOS 1; CHAIN: A;
SEQFOL	alos a							97.41									
PMF	score		0.45	0.62	-0.08							0.22					0.22
Verify	31036		0.26	0.59	0.04							10:0-					-0.03
Psi Blast			1.3e-11	6e-15	1.7e-49			1.7e-49				6.8e-91	-				3e-16
END	vv		204	217	704			741				415					1001
STAR			117	117	346			354				٥١					695
CHAI	7		∢		∢	WP-15 (-2		∢				¥		····			V
PDB	1		1114	3kvt	la12 .			1a12			-	la12					ldbn
SEQ	NO:		1528	1528	1529			1529				1529				202,	6751

SEQ SO	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										NUCLEOTIDE EXCHANGE FACTOR, GENE REGIT ATION
1529	lfao	∢.	930	1006	7.56-07	-0.27	0.33		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, A A A PETCH BENGTON BEOTEIN.
1529	1fb8	A	930	1007	3e-07	0.02	0.35		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, A DAPPON PROTEIN,
1529	siq i		935		0.0003	0.38	0.93		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
1529	Ipms		897	1004	1.5e-09	0.32	-0.02		SOS 1; CHAIN: NÜLL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1530	141j	Ą	2	138	6.8e-52	1.32	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POL Y-L- 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1530	IdIj	Ą	2	138	9e-63	1.32	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORMS CONTRACTION IN TRACTION IN TRACTION IN TRACTION OF THE PROFILIN IN THE PROFILIN I

PDB annotation	BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY	and the same of th			CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROCESSION OF THE PROTEIN.	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L- 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN, CONTRACTILE PROTEIN, CONTRACTILE PROTEIN.			MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE
Coumpound		PROFILIN; CHAIN: NULL;	PROFILIN; CHAIN: NULL;	ACTIN BINDING PROTEIN PROFILIN IPNE 3	ACTIN BINDING PROTEIN PROFILIN 1PNE 3		PROFILIN II; CHAIN: A, B, C, D;	PROFILIN II; CHAIN: A, B, C, D;	ACTIN BINDING PROTEIN PROFILIN IPNE 3	ACTIN BINDING PROTEIN PROFILIN IPNE 3	KINESIN; CHAIN: NULL;	KINESIN; CHAIN: NULL;
SEQFOL D score		-	167.69		167.40					133.14		
PIMF score		00'1		00'1			1.00	1.00	00.1		1.00	1.00
Verify score		1.04		0.92			0.75	0.71	0.64		-0.22	-0.15
Psi Blast		1.7e-52	1.7e-52	1.7e-52	1.7e-52		1.7e-42	4.5e-52	1.5e-42	1.5e-42	3e-68	6.8e-35
END		140	140	140	140	1	23	122	124	124	9/1	176
STAR T AA		2	7	2	2		71	2	2	2	2	2
CHAI N ID							∢	¥	•			
PDB TD		<u></u>	<u>1</u>	lpne	1pne		Idly	[ld]	Ipne	lpne	1bg2	16g2
SEQ B B SE		1530	1530	1530	1530		1531	1531	1531	1531	1534	1534

PDB annotation	ASSOCIATED	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL	PROTEIN; NCD CRYSTAL	STRUCTURE, MICROTUBULE	MOTORS, KINESIN 2 SUPERFAMILY,	MOTOR PROTEIN MOTOR PROTEIN	CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN,	CITOSNELETON	CONTRACTILE PROTEIN KINESIN, MICROTUBILE-BASED MOTOR.	NCD, CONTRACTED TEIN	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN, KAR3,	KINESIN-RELATED PROTEIN,	MOTOR 2 PROTEIN, ATPASE, P-	LOOP, MICROTUBULE BINDING	PROTEIN	MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	- Arten						AMINOTRANSFERASE AMINOTRANSEERASE AMINOTRANSEERASE	ENZYME
Coumpound		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C,	D;			KINESIN: CHAIN: A B.	Minder, Chan's to D,	KINESIN; CHAIN: A, B;	, ta	KINESIN MOTOR NCD; CHAIN: A:		KINESIN-LIKE PROTEIN KAR3;	CHAIN: NULL;			,	-	KINESIN HEAVY CHAIN;	CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	TRANSFERASE(AMINOTRANSF	ERASE) ASPARTATE	AMINOTRANSFERASE	(E.C.2.6.1.1) COMPLEXED WITH	1ARS 3 PYRIDOXAL-5'-	PHOSPHATE 1ARS 4	ASPARTATE AMMOTE ANSEER ASE: CHAIN:	A, B;
SEQFOL D score																												
PMF score		0.10				0.83	20.0	1.00		\$ 0 0		99.0						86.0		0.71	0.07						0.75	
Verify score		-0.36				0.03	50.0	-0.17		-0.24		-0.30						-0.25		-0.44	-0.22						0.17	
Psi Blast		le-17				3e-40	2	6.8e-19		5.8e-18		1.7e-21						1.5e-38		1.7e-20	6.8e-13						5.1e-81	
END AA		170				186	3	199	2	2		172						186		230	369						369	
STAR T AA		4				101		101		4-								105		105	71						-	
CHA1 N ID		Ą				ď	,	Д		₹			•					щ		മ		, 141					∢	
PDB ID		lcz7				2kin		2kin		7UCQ	-	3kar						3kin		3kin	lars						16jw	
SEQ UD NO:		1534				1534	1001	1534	1	4501		1534						1534		1534	1536						1536	

PDB annotation	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BLOSWITHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7- KETOPELARGONATE 3 SYNTHASE, TRANSFERASE	TRANSFERASE AONS, 8-AMINO-7- KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7- KEŢOPELARGONATE 3 SYNTHASE, TRANSFERASE	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5'-PHOSPHATE, PLP	TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C- 2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE.	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM, DECARBOXYLATION 2 INHIBITOR, LYASE	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM,
Coumpound	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	CYSTALYSN; CHAIN: A, B, C, D, E, F, G, H;	MALY PROTEIN; CHAIN: A, B;	2,2-DIALKYLGLYCINE DECARBOXYLASE (PYRUVATE); CHAIN: A;	2,2-DIALKYLGLYCINE DECARBOXYLASE
SEQFOL D score	69.72					169.86	
PMF score		0.12	0.16	0.25	-0.05		1.00
Verify score		0.32	0.09	-0.03	0.10		0.72
Psi Blast	1.7e-41	1.7e-41	6.8e-54	1.7e-18	3,4e-21	3.4e-63	3.4e-63
END	375	365	373	373	373	372	372
STAR T AA	parel .	47	1	89	92		46
CHAI N ID	◆	Ą	Ą	A	∀	Ą	¥
PDB ID	1550	1bs0	1bw0	1c7n	1d2f	ld7u	n/p1
SEQ NO:	1536	1536	1536	1536	1536	1536	1536

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PDB annotation	DECARBOXYLATION 2 INHIBITOR, LYASE	TRANSFERASE GABA-AT; PLP- DEPENDENT ENZYME, AMINOTRANSFERASE, 4- AMINOBUTYRIC ACID, 2	TRANSFERASE GABA-AT; PLP. DEPENDENT ENZYME, AMINOBUTYRIC ACID, 2 ANTHRI FPTIC DRIG TARGET	AMINOTRANSFERASE AMINOTRANSFERASE PYRIDOXAL-5'-PHOSPHATE, BIOTIN 2 BIOSYNTHESIS	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOMUTASE; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'- PHOSPHATE, 2 PYRIDOXAMINE-5'- PHOSPHATE, ASYMMETRIC DIMER	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOMUTASE; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'- PHOSPHATE, 2 PYRIDOXAMINE-5'- PHOSPHATE, ASYMMETRIC DIMFR	AMINOTRANSFERASE AMINOTRANSFERASE, 5- FLUOROMETHYLORNITHINE, PLP- DEPENDENT 2 ENZYME, PYRIDOX AI, PHOSPHATE	AMINOTRANSFERASE
Coumpound	(PYRUVATE); CHAIN: A;	4-AMINOBUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	4-AMINOBUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	7,8-DIAMINOPELARGONIC ACID SYNTHASE; CHAIN: A, B;	GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	ORNITHINE AMINOTRANSFERASE; CHAIN: A, B, C;	ORNITHINE
SEQFOL D score					90.43		130.71	
PMF score		1,00	1.00	1.00		1.00		1.00
Verify score		0.71	0.47	0.54		0.25		0.57
Psi Bļast		1.5e-70	1.7e-53	6.8e-64	1.2e-72	1.2e-72	1.7e-62	1.7e-62
END AA		370	373	371	372	372	372	369
STAR T AA		49	53	40	. ·	\$	2	40
CHAI N ID		∀	A	¥	¥	Ą	Ą	A
PDB ID		1gtx	1gtx	1qj5	2gsa	2gsa	2oat	20at
SEQ ID NO:		1536	1536	1536	1536	1536	1536	1536

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PDB annotation	AMINOTRANSFERASE, 5- FLUOROMETHYLORNITHINE, PLP- DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE	HYDROLASE SERCAI; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN	CHAPERONE HOP, TPR-DOMAIN.
Coumpound	AMINOTRANSFERASE; CHAIN: A, B, C;	CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPRZA-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;
SEQFOL D score					-			
PMF score		0.04	0.77	0.15	0.29	0.54	0.19	0.52
Verify score		-0.16	0.06	-0.35	-0.12	0.21	0.00	0.26
Psi Blast		0	3.40-23	1e-10	1.5e-13	1e-12	le-18	Ie-18
END AA		916	247	253	230	961	231	167
STAR T AA		91	135	179	102	101	139	
CHAI N ID		¥			щ	∢	Ą	A
PDB to		leul	la17	[a] 7	1e96	lelr	leir	leir
SEQ ID NO:		1539	1541	1541	1541	1541	1541	1541

SEQUENCE PUB CFIA STAR EAD Pul Blast Verify Store D Soure	-	_		-,																						
PDB CHAI STAR END Psi Blast Verify PMIF SEQFOL	PDB annotation		PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELLCAL REPEAT, HSC70, 2 HSP70, PROTEIN RINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL REPEAT HSC70 2 HSP70 PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMAIN,	REPEAT, HSC70, 2 HSP70, PROTEIN	BINDING	CHAPERONE HOP, TPR-DOMAIN,	PEPTIDE-COMPLEX, HELICAL	KEPEAT, HSC70, 2 HSP70, PROTEIN BINDING	SIGNALING PROTEIN	PEROXISMORE RECEPTOR 1, PTS1-	BP, PEROXIN-5, PTS1 PROTEIN.	PEPTIDE COMPLEX,	1 ELIKA I KICOPEPI I DE KEPEAT, TPR, 2 HELICAL REPRAT	PROTEIN TRANSPORT HELIX-	TURN-HELIX TPR-LIKE REPEAT,	PROTEIN TRANSPORT	TRANSFERASE	METHYLTRANSFERASE		STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN,
PDB CHAI STAR END Psi Blast Verify PMF Score	Coumpound		CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPRI-DOMAIN OF HOP; CHAIN:	A, B; HSC/0-FEF1IDE; CHAIN: C, D;	TPRI-DOMAIN OF HOP; CHAIN:	A, B; HSC70-PEPTIDE; CHAIN; C. D:	(; £;	TPRI-DOMAIN OF HOP; CHAIN:	C, D;		TPR1-DOMAIN OF HOP; CHAIN:	A, B; HSC70-PEPTIDE; CHAIN:		PEROXISOMAL TARGETING	SIGNAL 1 RECEPTOR; CHAIN:	A, B; PTS1-CONTAINING	PEPTIDE; CHAIN: C, D;		VESICULAR TRANSPORT	PROTEIN SEC17; CHAIN: A;		GLYCINE N-	METHYLTRANSFERASE;	CHAIN: A, B, C, D;	MJ0882; CHAIN: A;
PDB CHAI STAR END Psi Blast Verify Score	SEQFOL	D score																		63.04						
PDB CHAI STAR END Psi Blast Ps	PMF	score		0.53		0.01			0.46			0.37			0.18		•						-0.09		.	0.37
PDB CHAI STAR END Psi Blast	Verify	score		-0.04		0.30			0.73			0.35			-0.06								0.55			0.57
PDB CHAI STAR	Psi Blast			1.7e-20		3.4e-15			16-14						8.5e-35					3.4e-07				•	,	2
Ielw A	END	A.A		250		133	,		175			202	,		252					254			190		5	18/
PDB ID ID ID ID ID ID ID	STAR	TAA		133		28			2			86			. 9					7			65			7)
	CHAI	e z		∢		¥			∢			∢			₹					4	•		Ą			∢
SEQ ID NO: 1541 1541 1541 1541 1541 1541 1541 1542	PDB	a		leiw		lelw			lelw		,	Ielw			15g					1qqe			1d2h			Idus
	SEO	a ë		1541		1541			1541			1541			1541					1541			1542		16.65	7461

PDB annotation	METHANOCOCCUS JANNASCHII	TRANSFERASE RRNA	MEIHYLIKANSFEKANE EKMU, COFACTOR ANALOGS	METHYLTRANSFERASE GNMT, S-	ADENOSYL-L-METHIONINE\:	GLYCINE METHYLTRANSFERASE	METHYLTRANSFERASE TRANSFERASE	METHYLTRANSFERASE,	RESTRICTION SYSTEM	METHYLTRANSFERASE	METHVI TRANSFERASE	RESTRICTION SYSTEM	900	HYDROLASE TETRATRICOPEPTIDE,	PROTEIN-PROTEIN INTERACTIONS,	TPR, 2 SUPER-HELIX, X-RAY	SIRUCIURE SIGNAT ING BROTERI	PEROXISMORE RECEPTOR 1. PTS1-	BP, PEROXIN-5, PTS1 PROTEIN-	PEPTIDE COMPLEX,	TETRATRICOPEPTIDE REPEAT, TPR,	2 HELICAL REPEAT					·	
Coumpound		ERMC	METHYLIKANSFERASE; CHAIN: A;	GLYCINE N-	METHYLTRANSFERASE;	CHAIN: A, B;	ADENINE-N6-DNA- METHYL TRANSFER ASE TAOI:	CHAIN: A, B;		ADENINE-N6-DNA-	CHAIN: A R.			SERINE/THREONINE PROTEIN PHOCEPHATACE 5. CHAIN.	NULL;		PEROXISOMAI TAPGETING	SIGNAL I RECEPTOR: CHAIN:	A, B; PTS1-CONTAINING	PEPTIDE; CHAIN: C, D;			THE PROPERTY OF THE PROPERTY O	ANTERNIA DEDIA DE CATERI	THE LONG FIGURE AND TO SELLEN	WITH CYS 39 1AHD 3	REPLACED BY SER (C39S)	COMPLEX WITH DNA (NMR,
SEQFOL D score																							50 51	10.00		441-		
PMF score		00'0		-0.13			-0.14			0.16				0.28			0.25											
Verify score		0.27		-0.00			41.0			-0.29				-0.10			0.17										•	•
Psi Błast		3e-06		3.4e-17			5.1e-11			7.5e-06				1.5e-06			4.5e-06			-			< 1e_32	200				
END		200		061		5	261			337				58			83						201	<u> </u>				
STAR T AA		72		21			8			99				p-4			2						228	3				
CHAI N ID		٧		Ą			₹	. 		∢							4						۵	•				
PDB ID		Iqam		Ixva		1,00	E STORES			2adm				1a17		-	1 fch					1	1ahd	į		,		
SEQ ID NO:		1542		1542		1540	1347			1542				1544		**	1544						1545	}				

PDB annotation			COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTIONDNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS,
Coumpound	1AHD 4 16 STRUCTURES) 1AHD 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: B;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B;
SEQFOL D score				78.21			55.32	
PMF score		1.00	0.59		1.00	1.00		1.00
Verify score		0.01	-0.40		0.40	0.40		0.49
Psi Blast		5.1e-32	4.5e-22	3e-28	3e-28	5.1e-26	5.1e-27	5.1e-27
END		294	286	290	290	290	287	287
STAR T AA		229	212	224	233	233	226	233
CHAI N ID		a .	Ą	A	¥	Ą	₽	4
PDB ID		lahd	lau7	1b72	1672	1672	1b8i	168i
SEQ ID NO:		1545	1545	1545	1545	1545	1545	1545

			***************************************																	_	_	
PDB annotation	DEVELOPMENT, 2 SPECIFICITY													COMPLEX (DNA-BINDING	PROTEIN/DNA) HD;	HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) HD;	HOMEODOMAIN, COMPLEX (DNA-	BINDING PROTEIN/DNA)	CONDI BY (ZNIC BRICED (MAIA)	עיינים איינים נייושין יישם ויינים
Coumpound	DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3	REPLACED BY SER AND RESIDURS 1-6 DELETED	(C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	REPLACED BY SER AND	RESIDUES 1-6 DELETED	(C398,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	ANTENNAPEDIA PROTEIN;	CHAIN: A, B; DNA; CHAIN: C,	D, E, F;	ANTENNAPEDIA PROTEIN;	CHAIN: A, B; DNA; CHAIN: C,	D, E, F;		OGSP ZING FINGED DEPTINE.	לחווי לייייי ייייליייי לייייל
SEQFOL D score		59.53		57.26											·		61.44	•				
PMF score			0.92					1.00						1.00							1 00	
Verify score			-0.12					0.30						0.42							0.19	
Psi Blast		8.5e-28	8.5e-28	1.4e-29				1.4e-29						1.7e-29			1.7e-29				1 46-27	
END AA		296	294	291	-			294						288			288				6	
STAR T AA		227	229	234			.:	235	-					233			233		-		12	
CHAI N ID				,										∢			₩		,,		V	1
PDB ID		1ftz	7 1 11	1san				lsan						9ant			9ant				lalh	
SEQ ID NO:		1545	1545	1545				1545						1545			1545				1546	

PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
								CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	Ą	161	249	8.5e-27	0.26	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
	A	162	250	3e-28	0.16	0.88		OGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	A	199	277	1.5e-37	0.48	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	¥		49	5.1e-22	0.31	0.80		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	Ą	281	361	3.4e-30	0.22	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: R. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	Ą	309	391	3.4e-30			80.58	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	၁	101	185	I.5e-14	0.01	0.23		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA NTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
	သ	11	92	1e-46	0.48	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

WO 02/070539 PCT/US02/05095

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΑÖ	A	O N	TAA	AA		score	score	D score		
18.00									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	Imey	O	125	249	6e-25	-0.12	0.49		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
***************************************									PROTEIN: CHAIN: CHAIN:	FINGER, PROTEIN-DNA INTERACTION DROTEIN DESIGN 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1546	lmey	ပ	130	ដ	1.5e-39	-0.10	0.48		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									PROTEIN: CHAIN: C. F. G:	INTERACTION PROTFIN DESIGN 2
										CRYSTAL STRUCTURE, COMPLEX
		,								(ZINC FINGER/DNA)
1546	Imey	ပ	160	249	5.1e-47	0.09	00:1		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
•			-						PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
					~=.					CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	lmey	C	188	277	I.7e-47	0.57	1.00		DNA: CHAIN: A B D F:	COMPLEX (ZINC FINGER ONA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
		ļ		1						(ZINC FINGER/DNA)
1546	mey	ပ	 -	49	5.1e-34	0.26	0.95		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
				-					PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
-										CRYSTAL STRUGFORE, COMPLEX
				1						(ZINC FINGER/DNA)
1546	Imey	ပ်	224	305	le-49	0.81	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
			-							CRYSTAL STRUCTURE, COMPLEX
1546		C	1	†						(ZINC FINGER/DNA)
1340	Imey	ر	777	250	1e-49			105.23	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ	EDB CI	CHAI	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
.ö.									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER IDNA)
1546	lmey	U	252	333	1.2e-49	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
<u>1</u> 546	Ітеу	ပ	280	361	3.4e-49	0.38	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	် ပ	308	389	1.2e-49	0.37	00.1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN;-CHAIN: C, F, G;	COMPLEX (ZINC FINGER DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	Imey	Ų	336	411	3.4e-44	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	11ff6	A	132	291	1.4e-31	0.03	0.46		TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1466	¥	961	359	1.5e-37			117.50	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

WO 02/070539 PCT/US02/05095

d PDB annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	SS COMPLEX (TRANSCRIPTION ENB; REGULATION/DNASCEMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	SS COMPLEX (TRANSCRIPTION ENE; REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN		NO-COMPLEX (TRANSCRIPTION PS REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	
Coumpound		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENB; CHAIN: B, C, E, F;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YY1; CHAM; C; ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAM; A, B;	
SEQFOL D score						
PMF score		1.00	1.00	0.75	0.96	
Verify score		0.41	0.32	0.07	0.20	
Psi Blast		1.5e-3 <i>7</i>	1.5e-37	1.7e-26	6.8e-31	
END AA		342	403	410	249	
STAR		199	253	309	133	
CHAI N ID		•	∢	∢	U	
PDB ID		1476	1476	1476	lubd	
SEQ ID NO:		1546	1546	1546	1546	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB apportunities
Ş	2	•	.	ç		score	score	50%		
									ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
									CHAIN: A, B;	INITIATOR ELEMENT, YYI, ZINC 2
	_									FINGER PROTEIN, DNA-PROTEIN
										RECOGNITION, 3 COMPLEX
										(TRANSCRIPTION REGULATION/DNA)
1546	lubd	Ų	168	277	5.1e-33	0.47	1.00		YYI; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
	•			****					ASSOCIATED VIRUS PS	REGULATION/DNA) YING-YANG 1;
	-								INITIATOR ELEMENT DNA;	TRANSCRIPTION INITIATION,
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2
									•	FINGER PROTEIN, DNA-PROTEIN
										RECOGNITION, 3 COMPLEX
										TRANSCRIPTION
										REGULATION/DNA)
1546	Iubd	ပ	16	611	3e-25	0.24	0.81		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
									ASSOCIATED VIRUS P5	REGULATION/DNA) YING-YANG I;
_									INITIATOR ELEMENT DNA;	TRANSCRIPTION INITIATION,
					**************************************				CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2
					re-union		•			FINGER PROTEIN, DNA-PROTEIN
					•					RECOGNITION, 3 COMPLEX
_			•							(TRANSCRIPTION
╅		,	,							REGULATION/DNA)
1546	Jubd	ပ	6	150	1.7e-23	-0.28	0.16		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
-		****							ASSOCIATED VIRUS P5	REGULATION/DNA) YING-YANG 1;
			-		•				INITIATOR ELEMENT DNA;	TRANSCRIPTION INITIATION,
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2
				-						FINGER PROTEIN, DNA-PROTEIN
										RECOGNITION, 3 COMPLEX
										(TRANSCRIPTION
+	,									REGULATION/DNA)
1546	Inbd	ပ	-	87	3.4e-29	-0.01	8.		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
				,					ASSOCIATED VIRUS P5	REGULATION/DNA) YING-YANG 1;
7									INITIATOR ELEMENT DNA;	TRANSCRIPTION INITIATION,

PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score			97.53		
PMF score		1.00		1.00	1.00
Verify score		0.25		0.44	0.42
Psi Blast		7.5e-48	1.2e-50	1.2e-50	4.5e-47
END AA		333	334	362	389
STAR T AA		201	226	250	279
CHAI N ID		ن ن	U .	ပ	O O
PDB ID		1ubd	Iubd	lubd	lubd
SEQ ID NO:		1546	1546	1546	1546

PCT/US02/05095

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION	REGULATIONDNA) COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YANG 1; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YYL, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)		COMPLEX (DNA-BINDING
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII;
SEQFOL D score							
PMF score		1.00	1.00		0.93	0.74	0.68
Verify score		0.35	0.11		0.16	0.24	0.09
Psi Blast		1.7e-33	7.5e-46		8.5e-32	le-10	6e-32
END AA		389	417		410	122	150
STAR T AA		20 00 00 00 00	306		316		12
CHAI N ID		ပ	υ		ပ	•	Ą
PDB ID		1ubd	lubd		lubd	2drp	2gli
SEQ ID No:		1546	1546		1546	1546	1546

PCT/US02/05095

		т						
PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINGER	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL/11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
			106.53					
	0.34	0.94		1.00	0.95	1.00	00'1	0.99
	-0.08	0.34		0.35	0.40	0.13	0.45	0.14
	3.4e-26	3.4e-32	1.2e-63	1.2e-63	3.4e-34	9e-45	6.8e-31	1.5e-42
	248	304	363	391	388	418	410	279
	137	160	224	224	260	280	288	66
	¥	4	¥	Ą	4	Ą	¥	¥
	2gli	2gli	2gli	2gli	2gli	2gli	2gli	2gli
	1546	1546	1546	1546	1546	1546	1546	1546
		2gli A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	2gli A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; 2gli A 160 304 3.4e-32 0.34 0.94 ZINC FINGER PROTEIN GLII; 2gli A 160 304 3.4e-32 0.34 0.94 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D;	2gli A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; 2gli A 160 304 3.4e-32 0.34 0.94 ZINC FINGER PROTEIN GLII; 2gli A 224 363 1.2e-63 106.53 ZINC FINGER PROTEIN GLII; 2gli A 224 363 1.2e-63 106.53 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D;	2gii A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; CHAIN: C, D; 2gii A 160 304 3.4e-32 0.34 0.94 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D; 2gii A 224 363 1.2e-63 1.06.53 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D; 2gii A 224 391 1.2e-63 0.35 1.00 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	2gli A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D;	2gii A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D; CHA	2gli A 137 248 3.4e-26 -0.08 0.34 ZINC FINGER PROTEIN GLII; CHAIN: C, D; CHAI

PDB annotation	BINDING PROTEIN/DNA)	RIBOSOME 30S RIBOSOMAL	SUBUNIT, RIBOSOME, ANTIBIOTIC,	STREPTOMYCIN, 2	SPECTINOMYCIN, PAROMOMYCIN									•		- 70																		
Coumpound		16S RIBOSOMAL RNA; CHAIN:	A; FRAGMENT OF MESSENGER	KNA; CHAIN: X; 30S	RIBOSOMAL PROTEIN S2;	CHAIN: B; 30S RIBOSOMAL	PROTEIN S3; CHAIN: C; 30S	RIBOSOMAL PROTEIN S4;	CHAIN: D; 30S RIBOSOMAL	PROTEIN S5; CHAIN: E; 30S	RIBOSOMAL PROTEIN S6:	CHAIN: F; 30S RIBOSOMAL	PROTEIN S7; CHAIN: G; 30S	RIBOSOMAL PROTEIN S8;	CHAIN: H; 30S RIBOSOMAL	PROTEIN S9; CHAIN: 1; 30S	RIBOSOMAL PROTEIN S10;	CHAIN: J; 30S RIBOSOMAL	PROTEIN S11; CHAIN: K; 30S	RIBOSOMAL PROTEIN S12;	CHAIN: L; 30S RIBOSOMAL	PROTEIN S13; CHAIN: M; 30S	RIBOSOMAL PROTEIN S14;	CHAIN: N; 30S RIBOSOMAL	PROTEIN S15; CHAIN: O; 30S	RIBOSOMAL PROTEIN S16;	CHAIN: P; 30S RIBOSOMAL	PROTEIN S17; CHAIN: Q; 30S	RIBOSOMAL PROTEIN S18;	CHAIN: R; 30S RIBOSOMAL	PROTEIN S19; CHAIN: S; 30S	RIBOSOMAL PROTEIN S20;	CHAIN: T; 30S RIBOSOMAL	PROTEIN THX; CHAIN: V
SEQFOL D score				•																														
PMF score		1.00																																
Verify		0.78				-														-		,							<u>, , , , , , , , , , , , , , , , , , , </u>				-	
Psi Blast		le-53				•					•	•																						
END		366																					× 134.4				-	, -						
STAR T AA		217																											40-4-					
CHAI N ID		щ							•	•					-			-									_				_			
PDB ID		1fjg																												•				
SEQ NO ID		1547																-											-					

PDB aguacatur			TRANSCRIPTION INHIBITOR BETA- PROPELLER		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA NTER ACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	ZINC FINGEN DIVA)	EACTOD COL: 700 CONCED	TRANSCRIPTION ACTIVATION: SPI	ZINC FINGER TRANSCRIPTION	FACTOR SP1; ZINC FINGER,	TRANSCRIPTION ACTIVATION, SPI	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S
Coumpound	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN SS (PROKARYOTIC) 1PKP 3	RIBOSOMAL PROTBIN RIBOSOMAL PROTBIN S5 (PROKARYOTIC) 1PKP 3	TRANSCRIPTIONÁL REPRESSOR TUPI; CHAIN: A, B, C;	The Cities is a	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C. F. G:		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		SPIEZ: CHAIN: NIII 1:	of 112, Chain, NOLL,		SPIF2; CHAIN: NULL;	·		TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE;
SEQFOL D score	64.28	·			***************************************							legiago ana	****								
PIMF score	·	1.00	0.11	60.0	-0.20		0.09				0.18				-0.20	2		-0.13			0.07
Verify		0.53	0.31	2	0.02		-0.41				-0.05				0.21	į		0.05			-0.63
Psi Blast	1e-56	1e-56	0.0045	\$ 10.00	5.1e-29		5.1e-33				1.7e-07				1.7e-10)		8.5e-09			1.76-15
END	357	357	219	251	ī Ç		169				104				203	}		108			130
STAR T AA	211	217	119	170	7/1		77				77				173			78			8
CHAI N ID			A	c	د		ပ				ڻ ن		,	•					•		∢
PDB ID	1ркр	1pkp	lerj	1may	Imey		Imey				Iney	<u> </u>			1sp2			1sp2	-	5	2
SEQ ID NO:	1547	1547	1549	1553	5551		1553				1553				1553			1553		1000	ccci

PDB annotation	GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	LIGASE SKP2 F-BOX; SKP1; SKP1,
Coumpound	CHAIN: E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	SWIS; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	CYCLIN A/CDK2-ASSOCIATED
SEQFOL D score						54.61	
PMF score		0.24	0.00	0.36	0.03		0.41
Verify score		-0.83	-0.36	0.04	-0.30		-0.10
Psi Blast		1.46-15	5.1e-06	1.7e-06	3.4e-41	3.4e-41	4.5e-07
END AA		130	104	130	201	229	47
STAR T AA		49	78	74	52	79	∞
CHAI N ID		ပ		∢	A	А	A
PDB TD		Iubd	1zfd	2drp		2gli	1fs1
SEQ ID NO:		1553	1553	1553	1553	1553	1554

PDB U	CHAI	STAR T AA	END	Psi Blast	Verify	PIMF	SEQFOL D score	Coumpound	PDB annotation
								P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B. D.	SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, TRICH ITTIN DE OTERN 1 1754 SE
\vdash								,	
		-	99	3e-11	-0.49	0.24		CYCLIN H; CHAIN: NULL;	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
lqmz	В	۶	62	1.5e-09	-0.36	0.28		CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE ` PEPTIDE; CHAIN: E, F;	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN- DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX
-									
	4	122	541	0	0.02	0.78		ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING, 2 COMPLEX OF TWO FI ONGATION FACTORS
	₹	165	542	0		·	134.70	ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP- BINDING, 2 COMPLEX OF TWO FT ONGATION EACTORS
	A	122	548	0	0.41	1.00		ELONGATION FACTOR TU (EF. TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G PROFEIN, BETA-BARREL
	• 4	124	552	0			131.00	ELONGATION FACTOR TU (EF- TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
귀	¥	121	541	0	0.47	1.00		ELONGATION FACTOR;	RNA BINDING PROTEIN EFTU;

PDB annotation	TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN	RNA BINDING PROTEIN EFTU; TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)	HYDROLASE ERA, GTPASE, RNA- BINDING, RAS-LIKE, HYDROLASE		TRANSLATION EF-TU; GTPASE, MOLECULAR SWITCH, TRNA, RIBOSOME, Q-BETA REPLICASE, 2 CHAPERONE, DISULFIDE ISOMERASE	TRANSLATION PROTEIN-PROTEIN COMPLEX
Соитроина	CHAIN: A, B;	ELONGATION FACTOR; CHAIN: A, B;	BLONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	GTP-BINDING PROTEIN ERA; CHAIN: A, B;	TRANSPORT AND PROTECTION PROTEIN ELONGATION FACTOR TU (DOMAIN I) - *GUANOSINE DIPHOSPHATE IETU 4 COMPLEX IETU 5	ELONGATION FACTOR TU (EF- TU); CHAIN: A;	ELONGATION FACTOR EBF1A; CHAIN: A; ELONGATION
SEQFOL D score		129.64		115.68				
PMF			0.86		0.13	0.45	00.1	1.00
Verify			-0.05	•	0.05	0.18	0.29	0.31
Psi Blast		0	0	0	1.5e-13	8.5e-67	0	0
END AA		542	541	542	368	345	541	542
STAR TAA		137	122	172	126	118	117	120
CHAI N ID		A	¥	¥	¥	•	٧	Ą
PDB ID		lefc	lefu	lefu	lega	1etu	Іехш	1660
SEQ ID NO:		1559	1559	1559	1559	1559	1559	1559

Coumpound PDB annotation	FACTOR BEF1BA; CHAIN: B;	V FACTOR G; TRANSLATION EF-G; BENT CONFORMATION, VISIBLE DOMAIN III, MUTATION HISS73ALA	TRANSLATION INITIATION TRANSLATION TRANSLATIONAL FACTOR IF2/EIF5B; CHAIN: A; GTPASE		SERINE/THREONINE PROTEIN HYDROLASE TETRATRICOPEPTIDE, PHOSPHATASE, PHOSPHATASE, NULL; NULL; TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	SERINE/THREONINE PROTEIN HYDROLASE TECRACIOPER TIDE, PHOSPHATASE, PHOSPHATASE, NULL; PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE		EPTIDE	IN: B; REPEAT, HSP90, 2 PROTEIN BINDING	IN OF HOP; CHAPERONE HOP, TPR-DOMAIN,	EPTIDE					IN: B; KEPEAT, HSP90, 2 PROTEIN BINDING	
SEQFOL Co D score	FACTOR EEF	ELONGATION FACTOR G; CHAIN: A;	TRANSLATIC FACTOR IF2/		SERINE/THREONINE PRO PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PRO PHOSPHATASE 5; CHAIN: NULL;	TPR2A-DOMAIN OF HOP:	CHAIN: A; HS	MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-P; MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE MEEVD: CHAIN: B:	TPR2A-DOMAIN OF HOP;	CHAIN: A; HSP90-PEPTIDE	MEEVD; CHAIN: B;	
PMF		00:00	0.28		0.07	0.83	0.70		-	0.03		0.10		0.41			
Verify score		-0.15	0.03		0.08	-0.0 <u>I</u>	0.01			-0.46		-0.07		0.36			
Psi Blast		1.7e-05	8.5e-62		4.5e-09	1.2e-06	1.3e-08			0.0012	-	0.003		0.0003		•	
END		459	553		165	105	111			401		558		119			
STAR		319	123		19	7	19			316		462		54			
CHAI N ID		Ą	Ą			•	Ą			€.		Ý		₩.			
PDB CI		1fnm	lg7s	,	la17	1217	Ielr			lelr		leir		lelr			
SEQ ID NO:		1559	1559		1561	1561	1561			1561		1561		 1561			

		,	,			-		·
PDB annotation	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT. TPR.
Coumpound	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR I-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP: CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;
SEQFOL D score			·					,
PMF score		86.0	0.71	0.95	0.19	0.12	0.65	0.31
Verify score		0.38	0.26	0.31	-0.68	0.41	0.25	0.34
Psi Blast		7.5e-08	5.1e-06	4.5e-07	0.00034	1.7e-05	1.3e-13	1.2e-10
END AA		119	123	26	472	537	252	119
STAR T AA		19	25	2	382	458	17	2
CHAI N ID		∢	Y	4	A	Ą	¥	4
PDB ID		Ielw	lelw	leľw	lelw	lelw	Ifch	1fch
SEQ ID NO:		1561	1561	1561	1561	1561	1561	1561

	Γ		1	Γ				1		1
PDB annotation	2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 3 HEI ICA1 PEPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT		LIPID TRANSPORT APO A-1; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-	ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS,	SINOCIONAL INCIENT ENDOCYTOSIS/EXOCYTOSIS NOSCI; PROTEIN-PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35
Coumpound		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;		APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;		ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B.	SYNTAXIN-1A; CHAIN: A, B, C;
SEQFOL D score					68.91		68.37			
PMF		0.03	0.48					0.03	0.10	0.00
Verify score		0.05	0.10					0.04	-0.33	0.19
Psi Blast		3.4e-10	1.4e-11		1.4e-07		1.5e-10	1.5e-10	1.5e-13	1.5e-07
END AA		563	286		242		233	569	254	128
STAR T AA		31.8	31		4		<u>6</u>	61	81	5
CHAI N ID		Ą	4		¥.		∢	∢	ф	Ą
PDB ID		lfch	Ifch		lavi		lcun	leun	Idn1	lez3
SEQ ID NO:		1561	1561		1563		1563	1563	1563	1563

PDB annotation	KDA PROTEIN, P35A, THREE HELIX BUNDLE	PROTEIN TRANSPORT HELIX. TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE. HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION SIGMA70, RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION	COMPLEX (NHIBITOR/NUCLEASE) COMPLEX (NHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN
Coumpound		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L,
SEQFOL D score		90.09	71.18		·	·			
PMF score			-	-0.06	0.12	 0.00	0.62	-0.05	0.01
Verify score				0.01	0.09	 0.06	0.50	0.04	0.06
Psi Blast		1.2e-09	4.5e-17	4.5e-17	1.2e-06	1e-13	1.5e-13	6.8e-09	3,4e-15
END AA		283	291	246	287	143	176	133	140
STAR T AA		2	22	5	26	11	E.	43	æ
CHAI N ID		¥	Ą	¥		Ą	Ą	a .	Ą
PDB ID		1qqe	Iquu	Iquu	Isig	 1 a 4y	1a4y	1fo1	1fqv
SEQ ID NO:		1563	1563	1563	1563	1565	1565	1565	1565

	PDB annotation	A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS		
	Coumpound	i.	SKP2; CHAIN: A, C, E, G, 1, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.42.1.1) (50 MM TRIS, 2CBA 3 3 M AMMONIUM SULFATE, PH 7.8) 2CBA 4	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 MM TRIS, 2CBA 3 3 M AMMONIUM SULPATE, PH 7.8)
a districti Pilandina Pilandina	SEQFOL D score							403.66
	PMF score		0.99	0.07	0.03	0.35	1.00	
o deservició	Verify score	-	0.74	0.23	0.01	0.18	1.12	
	Psi Blast		3e-17	3.4e-15	1.5e-12	4.5e-10	0	O
	END		174	140	143	176	242	242
,	STAR T AA		۳.	m	guind quant	2	m	m
	CEAI N ID		¥	¥				
	PDB ID		lfqv	1682	2bnh	2bnh	2cba	2cba
	SEQ El SEQ		1565	1565	1565	1565	1567	1567

PDB annotation		OXIDOREDUCTASE COX-2,	CICLOOXIGENASE, PROSTAGI ANDIN	ARACHIDONATE, 2 ENDOPEROXIDE	OXIDOREDUCTASE HEME.	PROTEIN, PEROXIDASE,	OXIDOREDUCTASE, PEROXIDASE- 2 BROMIDE COMPLEX	OXIDOREDUCTASE HEME-	PROTEIN, PEROXIDASE,	OXIDOREDUCTADE COXIDASE-2	OVIDOREDITOTA SEL A DA CITEDONIO	ACID MEMBRANE PROTEIN	PEROXIDASE, DIOXYGENASE		OXIDOREDUCTASE ADR, NADPH:	ADRENODOXIN	OXIDOREDUCTASE;	FLAVOENZYME, MAD ANALYSIS,	ELECTRON TRANSFERASE	OXIDOREDUCTASE	FLAVOPROTEIN, OXIDASE	OXIDOREDUCTASE COMPLEX II;	COMPLEX II; COMPLEX II;	COMPLEX II; FUMARATE	REDUCTASE, COMPLEX II,	SUCCINATE DEHYDROGENASE, 2	RESPIRATION, OXIDOREDUCTASE	- Andrew PT	,
Coumpound	2CBA 4	PROSTAGLANDIN H2	MER. CHAIN: F.		MYELOPEROXIDASE; CHAIN:	A, B; MYELOPEROXIDASE;	CHAIN: C, D;	MYELOPEROXIDASE; CHAIN:	A, B; MYELOPEROXIDASE;	CHAIN: C, D;	PPOSTAGI ANDIN 112	SYNTHASE-1: CHAIN: A:	1		ADRENODOXIN REDUCTASE;	CHAIN: A;				SARCOSINE OXIDASE; CHAIN:	A, B;	FUMARATE REDUCTASE	FLAVOPROTEIN SUBUNIT;	CHAIN: A, M; FUMARATE	REDUCTASE IRON-SULFUR	PROTEIN; CHAIN: B, N;	FUMARATE REDUCTASE 15 KD	HYDROPHOBIC PROTEIN;	CHAIN: C, U; FUMAKA I E REDUCTASE 13 KD
SEQFOL D score										-				•									•						
PIMF score		-0.11			0.19			1.00			1 00	20:1			0.00					0.81		0.03							
Verify score		90.0			-0.76			0.61			0.22	77.0			-0.65					0.31		-0.04							
Psi Blast		0			3.4e-41			0			0	>			0.0045					6.8e-37		8,5e-53							
END AA		089			241			714			680	3			82					430		437							
STAR T AA		167			139			252			167	<u> </u>			51					62		19							
CHAI N ID		Ą			Ą			ပ			•	¢			₹					Ą		¥							
PDB ID		lcvu		_	1d2v	•		1d2v	der die	- Lines Evilen	1 div	ì			1cjc					lels	,	Ifum							
SEQ ID NO:		1568			1568			1568			1568	3			1569					1569	1	1569						-34.	

			T	T			7		
PDB annotation			OXIDOREDUCTASE FUMARATE REDUCTASE, SUCCINATE DEHYDROGENASE, RESPIRATORY 2 CHAIN, CITRIC ACID CYCLE, FLAVOPROTEIN, IRON-SULPHUR 3 PROTEIN, DIHAEM CYTOCHROME B	OXIDOREDUCTASE OXIDOREDUCTASE		ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORYLATION	ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORYLATION	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN CALPONIN
Coumpound	HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LPF 3 FLAVIN-ADENINE- DINUCLEOTIDE (FAD) 1LPF 4	FUMARATE REDUCTÁSE FLA VOPROTEIN SUBUNIT; CHAIN: A, D; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, E; FUMARATE REDUCTASE CYTOCHROME B SUBUNIT; CHAIN: C, F;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A. D:	OXIDOREDÚCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	T-FIMBRIN; CHAIN: NULL;	T-FIMBRIN; CHAIN: NULL;	UTROPHIN; CHAIN: A, B;	UTROPHIN; CHAIN: A, B;
SEQFOL D score							t	74.32	
PIMF score		0.07	40.0	-0.09	0.09	0.83	0.40		1.00
Verify score		-0.23	-0.34	0.04	60'0-	0.60	0.54		0.84
Psi Blast		0.003	1.2e-43	8,5e-29	0.0015	5.1e-24	1.5e-29	4.5e-35	1.7e-34
END		82	437	434	83	230	230	232	232
STAR T AA		46	61	28	46	125	127	123	126
CHAI N ID		A	Α .	Ą	A			Ą	Ą
PDB ID		11pf	Iqla	1908	3lad	laoa	1aoa	1bhd	Ibhd
SEQ TD NO:		1569	1569	1569	1569	1571	1571	1571	1221

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PDB annotation	HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON	ACTIN-BINDING CALPONIN HOMOLOGY (CE) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN- BINDING, UTROPHIN	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN		LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIOUITIN CONJUGATING ENZYME	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJIGATING ENZYME	CELL ADHESION NCAM; NCAM,
Coumpound		UTROPHIN; CHAIN: A, B;	SPECTRIN BETA CHAIN; CHAIN: A;	SPECTRIN BETA CHAIN; CHAIN: A;	DYSTROPHIN; CHAIN: A, B, C, D;	UTROPHIN ACTIN BINDING REGION, CHAIN: A, B;		UBIQUITIN-PROTEIN LIGASE E34; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2: CHAIN: D;	UBIQUITIN-PROTEIN LIGASE E34; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2: CHAIN: D:	NEURAL CELL ADHESION
SEQFOL D score	-		86.88						131.07	
PMF score		1.00		1.00	1.00	1.00		1.00		0.05
Verify score		0.85		0.86	69:0	0.68		0.24		0.66
Psi Blast		4.5e-35	8.5e-43	8.5e-43	16-35	5.1e-35		0	O	1e-06
END		232	235	235	233	233		562	564	207
STAR T AA		127	126	127	126	126		202	212	115
CHAI N ID		Ą	Ą	¥	¥	∢		∢	4	Ą
PDB ID		phdi	lbkr	1bkr	1 dxx	lqag		1642	1042	lepf
SEQ No:		1571	1571	1571	1571	1571		1574	1574	1575

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PDB annotation	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMA INS. B-TREFOIL FOLLD		IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN 1G REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR,
Coumpound	MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	TLYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	TITIN, 127; CHAIN: NULL;	FC GAMMA RIIB; CHAIN: A;	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A:	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	SIALIDASE; CHAIN: NULL;	SIALIDASE; CHAIN: NULL;	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B:	GROWTH HORMONE, CHAIN: A; PROLACTIN RECEPTOR;
SEQFOL D score											53.09
PMF score		0.13	0.04	0.00	0.01	-0.19	-0.20	-0.20	-0.19	-0.14	
Verify score		-0.30	0.13	-0.25	0.13	0.08	0.14	0.05	0.03	0.02	
Psi Blast		3e-0 <i>5</i>	1.5e-06	1.2e-05	7.5e-06	9e-10	7.5e-10	1.5e-10	6e-10	6e-11	6e-11
END AA		188	212	186	206	999	643	324	476	212	224
STAR T AA		113	115	113	105	484	491	138	266	102	31
CHAI N ID		ជ	Ą		A	Ą	A			В	В
FDB ID		Iev2	1hng	‡‡	2fcb	1d0s	1d0s	leut	leut	1bp3	1bp3
SEQ ID NO:		1575	1575	1575	1575	1576	1576	1576	1576	1578	1578

	FUB annotation	HORMONE/GROWTH FACTOR	CONNECTIN A71, CONNECTIN;	TITIN, CONNECTIN, FIBRONECTIN TYPE III		IN; SANDWICH, CYTOKINE RECEPTOR,	ATUMOR CALL	TLA TLA		AGMENT	FB3 I WO		IDUES	HORMONE/GROWTH		-	 COMPLEX, FN 2 III DOMAINS, BETA	SHEET DOMAINS, CYTOKINE-		VIII.I CELL ADHESION PROTEIN CELL		FXTRACELLIII AR MATRIX 2	HEPARIN-BINDING	GLYCOPROTEIN		EXTRACELLIL AR MATRIX 2
	Coumpound	CHAIN: B;	TITIN; CHAIN: NULL;		CYTOKINE RECEPTOR	COMMON BETA CHAIN;	NEURAL ADHESION	MOLECULE DROSOPHILA	NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT	CONTAINING THE ICEBS 1 WO AMINO PROXIMAL	FIBRONECTIN TYPE III	REPEATS ICFB 4 (RESIDUES	PLACENTAL LACTOGEN:	CHAIN: A, PROLACTIN	RECEPTOR; CHAIN: B, C;			FIBRONECTIN; CHAIN: A;	FIBRONECTIN: CHAIN: NIII.I.					FIBRONECTIN; CHAIN: NULL;	
x04040	SEQFOL D score									-	-								56.61	57.30						
	score		80.0-		-0.09		0.04							-0.14											0.34	
XI.	score		-0.00	-	90.0		0.09							0.23											0.30	
10.00	rsi biasi		96-10		36-08		6e-10							36-10					7.5e-06	1.2e-09		•			1.2e-09	
C. W.	AA		218		211		199							211					315	224					661	
ST. LT.	TAA		119		124		41							124					35	34					37	
17100	NID				A									В					∢		•					
ana	a a		1bpv		1c8p		1cfb							1f6f			 		uu.	1mfn					1mfn	
043	Sec.		1578		1578		1578							1578					1578	1578					1578	

PDB annotation	GLYCOPROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN		PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE,	EUBACHEKIAL Z AMINOGLYCOSIDE RESISTANCE	GCN5-RELATED N-	ACETYLTRANSFERASE, 3 COA- BINDING	TRANSFERASE N-ACETYL	IKANSFEKASE	TRANSFERASE PROTEIN-ACETYL	COENZYME A COMPLEX, ACETYLTRANSFERASE	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX,	ACETYLTRANSFERASE	
Coumpound		TENASCIN; CHAIN: A, B;	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	FIBRONECTIN; CHAIN: A;	ARYLALKYLAMINE N. ACETYLTRANSFERASE; CHAIN: A, B;	SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N-	CITAIN: A, B;			SEROTONIN N-	CHAIN: A;	HPA2 HISTONE	ACELYLIKANSFEKASE; CHAIN: A, B, C, D;	HPA2 HISTONE ACETYLTRANSFERASE;	CHAIN: A, B, C, D;	
SEQFOL D score		55.27									, š.		•			
PMF			0.59	0.10	0.80	0.10				98.0		0.04		0.00		
Verify score			-0.03	0.11	0.42	-0.56				0.50		-0.15		0.08		
Psi Blast		4.5e-07	1,5e-09	9e-10	8.5e-14	1.7e-10				5.1e-13		5.1e-12		1.5e-14		
END		211	199	213	627	622				627	-	624		633		
STAR T AA		35	124	124	511	523				511		487		537		
CHAI N ID		∢		∢	B	• *				₹	(1)	4		∢		
PDB ID		1qr4	1111	2finb	Ib6b	1504				lcjw		1qsm		1qsm		
SEQ No.		1578	1578	1578	1579	1579				1579		1579		1579		

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PDB annotation	TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AAC; AMINOGLYCOSIDE 6-N- ACETYLTRANSFERASE, ANTIBIOTIC 2 REDECEMEN, ACETYL COENTYME A	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2 AMINOGLYCOSIDE RESISTANCE, GCN5-RELATED N- ACETYLTRANSFERASE, 3 COA- BINDING	TRANSFERASE N-ACETYL TRANSFERASE	SIGNALING PROTEIN P300/CBP ASSOCIATED FACTOR, COENZYME A, ACETYLTRANSFERASE, 2 COACTIVATOR, SIGNALING PROTEIN	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYL TRANSFERASE	TRANSFERASE PROTEIN-ACETYL COBNZYME A COMPLEX, ACETYL TRANSFERASE	TRANSFERASE HISTONE ACETYLTRANSFERASE, GCN5- RELATED N- ACETYLTRANSFERASE, 2 COA BINDING PROTEIN
Coumpound	ARYLALKYLAMINE N- ACETYLTRANSFERASE; CHAIN: A, B;	AMINOGLYCOSIDE N6- ACETYLTRANSFERASE TYPE 1; CHAIN: A;	SERRATIA MARCESCENS AMINOGL YCOSIDE-3-N- CHAIN: A, B;	SEROTONIN N. ACETYLTRANSFERASE; CHAIN: A;	P300/CBP ASSOCIATING FACTOR; CHAIN: B, A;	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D:	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A. B. C. D:	TGCNS HISTONE ACETYL TRANSFERASE; CHAIN: A;
SEQFOL D score								
PMF score	0.83	0.16	0.04	0.63	0.10	0.64	0.00	0.48
Verify score	0.43	-0.18	0.18	0.59	0.13	0.17	0.08	-0.21
Psi Blast	3.4e-19	1.7e-11	5.1e-12	1.5e-18	le-17	3.4e-11	1.5e-14	8.5e-16
END AA	732	749	727	732		729	738	749
STAR T AA	616	626	627	610	637	615	642	637
CHAI N ID	g Ω	∢	• •	A	B	∀ ·	Ą	¥
PDB ID	1565	1587	1bo4	1cjw	1cm0	1qsm	Iqsm	Iqst
SEQ ID NO:	1580	1580	1580	1580	1580	1580	1580	1580

PCT/US02/05095

PDB annotation	GENE REGULATION ADA4; TRANSCRIPTIONAL REGULATION, HISTONE ACETYLATION, N-2 ACETYLTRANSFERASE, GCN5 RELATED N-ACETYLTRANSFERASE FAMILY, 3 GENE REGULATION	OXIDOREDUCTASE TRYPANOTHIONE REDUCTASE, FAD DEPENDENT DISULPHIDE 2 OXIDOREDUCTASE	OXIDOREDUCTASE FLAVIN- DEPENDENT AMINE OXIDASE, OXIDOREDUCTASE		RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE,
Coumpound	TRANSCRIPTIONAL ACTIVATOR GCNS; CHAIN: A, B;	TR YPANOTHIONE REDUCTASE; CHAIN: A, B;	POLYAMINE OXIDASE; CHAIN: A, B, C;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN
SEQFOL D score							
PMF score	0.39	0.21	0.09	0.16	0.63	0,93	0.33
Verify score	-0.37	0.06	0.02	0.01	0.48	0.50	0.50
Psi Blast	5.1e-14	1.2e-06	0.00014	1.5e-07	1.4e-13	3.4e-11	1.7e-11
END AA	749	116	104	123	126	122	126
STAR T AA	637	65	70	67	44	40	4.
CHAI N ID	4	¥	Ą	∢	Ą	A	A
PDB ID	lygh	laog	1b37	3lad	1634	1534	143b
SEQ ID NO:	1580	1582	1582	1582	1587	1587	1587

PDB annotation	RNA BINDING PROTEIN	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN		OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
Coumpound	ASSOCIATED CHAIN: B, D, F, H, J, L;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, I, L.	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, J, L;	-	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE: CHAIN: B;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	INTERLEUKIN 16; CHAIN: NULL;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;
SEQFOL D score									
PMF score		0.99	69.0		96'0	0.82	1.00	0.76	0.93
Verify score		0.25	0.26		0.69	0.72	0.56	0.35	0.83
Psi Blast		5.1e-24	8.5e-25		3e-14	3,4e-13	1.5e-18	1.5e-16	7.5e-15
END		134	134	-	80	110	98	96	82
STAR T AA		43	39		12	¢,	<i>ب</i>	5	6
CHAI N ID		В	Q		Ą	Ą	¥		Æ
PDB ID		1d3b	1436		1b8q	1b8q	1be9	1116	Ikwa
SEQ ID NO:	_	1587	1587		1588	1588	1588	1588	1588

PDB annotation	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT	OXIDOREDUCTASE BETA-FINGER	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING	PROTEIN BINDING GATE-16; UBIQUITIN FOLD	LIPID TRANSPORT APO A-1; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCIEROSIS, HDL, LCAT- ACHIVATION	STRUCTURAL PROTEIN TWO- REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN
Coumpound	HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	TYROSINE PHOSPHATASE (PTP-BAS, TYPE I); CHAIN: A;	GOLGI-ASSOCIATED ATPASE ENHANCER OF 16 KD; CHAIN: A, B;	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score							54.19	61.70
PIMR score	1.00	0.95	1.00	0.99	1.00	0.89		
Verify score	0.78	0.89	0.66	0.79	0.91	0.36		
Psi Blast	16-17	1.2e-14	3.4e-19	1.4e-15	1.7e-16	8.5e-34	4.5e-06	1.5e-07
END AA	06	96	81	83	98	187	244	248
STAR T AA	m	12	3		3	91	29	28
CHAI N ID		¥	Ą	Ą	A	4	4	• ∢
PDB ID	1 pdr	1qau	Iqav	1qic	3pqz	1606	lav1	lcun
SEQ D NO:	1588	1588	1588	1588	1588	1590	1591	1591

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PDB annotation	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COIL, CONTRACTILE PROTEIN	TRANSPORT PROTEIN VAMP 2; MEMBRANE FUSION PROTEIN COMPLEX, TRANSPORT PROTEIN	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	COMPLEX (BLOCK) COAGULATION/INHIBITOR)	AUTOPROTHROMBIN IIA; HYDROLASE, SERINE	PROTEINASB), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COMPLEX (BLOOD COAPLEX (BLOOD COAGULATION/RHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN,
Coumpound	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	SSOI PROTEIN; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	SYNAPTOBREVIN 2; CHAIN: A, E, I; SYNTAXIN 1A; CHAIN: B, F, J; SNAP-25B; CHAIN: C, G, K; SNAP-25B; CHAIN: D, H, L;	DHP1; CHAIN: NULL;	DHP1; CHAIN: NULL;	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI;	CHAIN: F;		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;
SEQFOL D score				57.26	55.15						
PMF	0.45	0.95	0.04			0.16	0.17	90.0		-	0.47
Verify score	-0.00	0.16	0.23			0.49	0.17	0.21	·		0.32
Psi Blast	3.4e-22	1.5e-38	3,4e-13	4.5e-12	9e-24	5.1e-05	3.4e-05	1e -10			4.5e-12
END	233	233	213	251	245	73	75	324			385
STAR T AA	17	19	22	28	174	30	36	249			306
CHAI N ID	В	æ	¥	Ą	8			ا ا	•		L
PDB ID	ldnl	Idn1	1fio	nnbl	1sfc	4hb1	4hb1	laut			laut
SEQ ID NO:	1591	1591	1591	1591	1591	1651	1591	1592			1592

PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR)	SURFACE PROTEIN MEROZOITE	SURFACE ANTIGEN I, MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN,	EXTRACELLULAR, MODULAR	PROTEIN, SURFACE 2 ANTIGEN,	MALARIA VACCINE COMPONENT, SURFACE PROTEIN	SURFACE PROTEIN MEROZOITE	SURFACE ANTIGER 1, MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN.	EXTRACELLULAR, MODULAR	PROTEIN, SURFACE 2 ANTIGEN,	MALARIA VACCINE COMPONENT,	SURFACE PROTEIN	BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)		BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)	-	BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)	
Coumpound		MEROZOITE SURFACE	PROTEIN 1; CHAIN: A;					MEROZOITE SURFACE	PROTEIN 1; CHAIN: A;						BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOKOME I HYLKE I ONE	(DIFNCIMA) WILD COMIN. C,
SEQFOL D score																																
PMF score		0.04						0.04							0.09	,					0.19						0.16					
Verify score		81.0						90:0							0.44						0.17					,	0.02					
Psi Blast		1.5e-09						1.5e-14							1.4e-09						3.4e-11						3e-15					
END AA		326						374							981						249						385					
STAR T AA		246						280							109						139						253					
CHAI N ID		¥						٧		•	•				-1						_1						 -l					
PDB 11		lej.						lcej							ldan		-		-	1	dan				- X		1dan					
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PDB annotation		HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE	COMPLEX				HYDROLASE/HYDROLASE	INHIBITOR PROTEIN-PEPTIDE	COMPLEX				SERINE PROTEINASE	COAGULATION FACTOR II;	COAGULATION FACTOR II;	FETOMODULIN, TM, CD141	ANTIGEN; EGR-CMK SERINE	PROTEINASE, EGF-LIKE DOMAINS,	ANTICOAGULANT COMPLEX, 2	ANTIFIBRINOL YTIC COMPLEX	SERINE PROTEINASE	COAGULATION FACTOR II;	COAGULATION FACTOR II;	FETOMODULIN, TM, CD141	ANTIGEN; EGR-CMK SERINE	PROTEINASE, EGF-LIKE DOMAINS,	ANTICOAGULANT COMPLEX, 2	ANTIFIBRINOL YTIC COMPLEX	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE
Coumpound	-	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I;	DES-GLA FACTOR VIIA (LIGHT	CHAIN); CHAIN: L, M; (DPN)-	PHE-ARG; CHAIN: C, D;	PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA	(HEAVY CHAIN); CHAIN: H, I;	DES-GLA FACTOR VIIA (LIGHT	CHAIN); CHAIN: L, M; (DPN)-	PHE-ARG; CHAIN: C, D;	PEPTIDE E-76; CHAIN: X, Y;	THROMBIN LIGHT CHAIN;	CHAIN: A, B, C, D; THROMBIN	HEAVY CHAIN; CHAIN: M, N,	O, P; THROMBOMODULIN;	CHAIN: I, J, K, L, THROMBIN	INHIBITOR L-GLU-L-GLY-L-	ARM; CHAIN: E, F, G, H;		THROMBIN LIGHT CHAIN;	CHAIN: A, B, C, D; THROMBIN	HEAVY CHAIN; CHAIN: M, N,	O, P; THROMBOMODULIN;	CHAIN: I, I, K, L; THROMBIN	INHIBITOR L-GLU-L-GLY-L-	ARM; CHAIN: E, F, G, H;		FIBRILLIN; CHAIN: NULL;	-				
SEQFOL	D score																																	
PMF	score	-0.03					-0.18						0.01								-0.15								-0.05					
Verify	score	0.24					0.13						-0.18								0.03								0.01			•		
Psi Blast		1.4e-09					3.4e-11						1.2e-14								8.5e-12								1.7e-09					
END		186					249						383								\$								339					
STAR	T AA	601		٠			139						295			-					307								245					
CHAI	al N	٦ •					 						-													•			·					
FDB	a	1dva					ldva						TdxS.								Idx5								lemn					
SEO	a ö	1592					1592						1592								1592						,=		1592					

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PDB annotation	DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY, DISEASE MITTATION 3 EGE, 172	DOMAIN HIMAN FIRM I N-1	FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING	PROTEIN	BLOOD CLOTTING	COMPLEX(SERINE	PROTEASE/COFACTOR/LIGAND),	BLOOD COAGULATION, 2 SERINE	PROTEASE, COMPLEX, CO-FACTOR,
Coumpound		FIBRILLIN; CHAIN: NULL;						FIBRILLIN; CHAIN: NULL;								FIBRILLIN; CHAIN: NULL;						-		TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;		BLOOD COAGULATION	FACTOR VIIA; CHAIN: L;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: H;	SOLUBLE TISSUE FACTOR;
SEQFOL D score		56.86		-													•							55.46							
PMF score								0.55								0.13											0.03				
Verify score								0.33								0.36			•								0.0				
Psi Blast		1.7e-15						1.7e-15								8.5e-14								3e-10			1.4e-09				
END		382						380								402		٠						357		1	 98 				
STAR T AA		277						302								337								194			109				
CHAI N ID	-					******									1				_					4							
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SEQ ID NO:		1592						1592								1592								1592			1592				

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PDB annotation	RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	BLOOD CLOTTING COMPLEX(SERINE	BLOOD COAGULATION, 2 SERINE	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR.	GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	HORMONE RECEPTOR HORMONE	RECEPTOR, INSULIN RECEPTOR FAMILY	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF.	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR) CHRISTIMAS FACTOR: COMPLEX.						
Coumpound	CHAIN: T; SL15; CHAIN: I;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L;	FACTOR VIIA; CHAIN: H;	SOLUBLE TISSUE FACTOR; CHAIN: T; SL15; CHAIN: I;		INSULIN-LIKE GROWTH	FACTOR RECEPTOR 1; CHAIN: A;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;						FACTOR IXA; CHAIN: C, L., D-	PHE-PRO-ARG; CHAIN: I;
SEQFOL D score	·											70.13	"										
PMF score		-0.18				0.00		0.31	-0.12	-0.14	-0.18		-0.14	-0.19	-0.12						;	-0.07	
Verify score		0.08				0.20		0.15	0.44	0.29	0.19		0.37	0.07	0.58							0.44	
Psi Blast		3.4e-11				4.5e-12		3.4e-13	3.4e-18	7.5e-19	3.4e-17	7.5e-19	3.4e-12	ie-11	3.4e-09		•			٠		1.5e-10	
END		249				380		242	281	331	382	396	193	403	E73	-	•				000	677	
STAR T AA		139	•			246		112	146	147	230	231	27	295	109						000	139	
CHAI N ID		⊢				¥									<u>ــ</u>								•
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PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	PLASMINOGEN ACTIVATION	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD
Coumpound		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN), CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CFAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score							
PMF		-0.09	-0.17	-0.18	0.71	-0.05	-0.12
Verify score		0.55	0.23	0.26	0.49	0.91	0.23
Psi Blast		1.4e-09	3.4e-10	7.5e-09	1.3e-11	3e-10	3.4e-09
END		186	249	338	385	180	189
STAR T AA		109	143	253	283	128	109
CHAI N ID		ы		⊣	<u>.</u>		ľ
PDB ID		1qfk	1qfk	1 0 fk	1qfk	1tpg	1xka
SEQ NO:		1592	1592	1592	1592	1592	1592

PDB annotation	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR	STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE	PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR: BLOOD	COAGULATION FACTOR, SERINE	PROTEINASE, EFIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR	STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE	FROIEINASE, EFIDERMAL 2 GROWTH FACTOR LIKE DOMAIN										CHAPERONE HSP40; CHAPERONE,	DNAK
Coumpound		BLOOD COAGULATION	FACTOR AR; CHAIN: L, C;		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;			BLOOD COAGULATION	FACTOR XA; CHAIN: L, C;			LECTIN (AGGLUTININ) WHEAT	GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT	GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT	GERM AGGLUTININ	I FORDI (1 GOT I FINE A)	CECLIN (AGGLOLININ) WHEAT	(ISOLECTIN 2) 9WGA 3	DNAJ; CHAIN: NULL;	
SEQFOL D score								53.26						60.84							81.78	
PMF		-0.03			0.46							-0.12				-0.19		200	cn.u-			
Verify score		0.04			0.43							0.22				0.04		6	20.0-			
Psi Blast		7.5e-09			1.2e-11			1.2e-11				3.4e-14		1.5e-16		1.4e-15		2 40.12	5.46-13		3.4e-28	
END		328	44.4		382			362				264	·	340		342		100	177		11	
STAR T AA		255			283			305				114	_	152		183		8	76			
CHAI N ID		ı			∟			L •				Ą		Ą		Ą			<			
PDB ID		lxka			lxka			1xka			•	9wga		9wga		9wga		D. F. Car	A A KA		1590	
SEQ ID NO:		1592			1592			1592				1592		1592		1592	************	1505	2601		1593	

													-										
PDB annotation	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	MOLECULAR CHEPERANE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE					COMPLEX (DNA-BINDING	PROTEIN/DNA)	والمراجعة				M		GENE REGULATION/DNA LEF-1	HMG; LEF1, HMG, TCR-A,	TRANSCRIPTION FACTOR, DNA	BINDING, DNA 2 BENDING,	COMPLEX (HMG DOMAIN/DNA),	GENE REGULATION/DNA	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A,
Coumpound	DNAI; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	DNA-BINDING HIGH MOBILITY GROUP PROTEIN	FRAGMENT-B (HMGB) (DNA-	DOMAIN B OF RAT HMG1)	(NIMR, 1 STRUCTURE) 1HME 4	HUMAN SRY; 1HRY 6 CHAIN:	A; 1HRY 7 DNA; 1HRY 9 CHAIN: B; 1HRY 10	DNA-BINDING HIGH	MOBILITY GROUP PROTEIN 1	(HMG1) BOX 2, COMPLEXED UTTH 1 HSM 3	WILL HOM S MERCAPTOETHANOLONM	MINIMIZED AVERAGE	STRUCTURE) 1HSM 4	LYMPHOID ENHANCER-	BINDING FACTOR; CHAIN: A;	DNA (5'- CHAIN: B; DNA (5'-	CHAIN: C;		and the second s	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A;
SEQFOL D score		86.98													_		125.69						
PIMIF	0.1		1.00	1.00	0.43				0.24		0.75												1.00
Verify score	0.84		26.0	26:0	-0.13				0.01		0.11												0.31
Psi Blast	3.4e-28	16-33	3.4e-27	16-33	1.4e-21				1e-27		3.4e-22						3e-22						3e-22
END	89	78	89	77	416				416		419						429						420
STAR T AA	es .	2	8	3	351				350		351						344						345
CHAI N ID			•						∢.								∢					_	&
PDB IID	15q0	1hdj	Ihdj	1hdj	1hme				lhry		1hsm						2lef						2let
SEQ NO:	1593	1593	1593	1593	1594				1594		1594						1594						1594

PDB annotation	TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAN/DNA), GENE REGIT ATTON/DNA		DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN	COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA)	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGHT ATTON/DNA	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING,
Coumpound	DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;		NON HISTONE PROTEIN 6 A; CHAIN: A;	HUMAN SRY; 1HRY 6 CHAIN: A; 1HRY 7 DNA; 1HRY 9 CHAIN: B: 1HRY 10	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B: IHRY 10	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	LYMPHOID ENHANCER- BINDING FACTOR, CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5- CHAIN: B; DNA (5- CHAIN: C;
SEQFOL D score				÷		83.75		57.47	
PMIF score		1.00		0.89	0.78		0.81		0.74
Verify score		0.40		0.10	-0.10		0.04		-0.29
Psi Blast		3.4e-20	•	8.5e-21	1e-21	7.5e-27	7.5e-27	6e-27	8.5e-17
END		420		901	114	115	115	128	128
STAR T AA		350		31	43	43	44	£ 3	44
CHAI N ID		¥		Ą	Ą	A	A	∢	Ą
PDB		2lef		lcg7	lhry	lhry	Ihry	2lef	2lef
SEQ	Ö	1594		1598	1598	1598	1598	1598	1598

PDB annotation	COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX	(TRANSDUCER/TRANSDUCTION)	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	STRUCTURAL PROTEIN EF-HAND LIKE DOMAIN, WW DOMAIN			
Coumpound		LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;		FORMIN BINDING PROTEIN; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	DYSTROPHIN; CHAIN: A;			
SEQFOL D score								·			
PMF score		0.71	-0.20		96.0	0.94	06'0	96.0	0.87	0.35	0.22
Verify score		0.27	0.10		0.60	0.72	0.17	60.0	0.03	0.64	0.27
Psi Blast		6e-27	1.5e-09		5.le-07	1.5e-09	3e-09	8.5e-08	3.4e-09	3.4e-12	3.4e-06
END AA		116	173		160	161	121	121	159	118	117
STAR T AA		45	o.		133	133	87	92	129	85	23
CHAI N ID		∢	o.		Ą	¥	Ą	A	¥	Ą	¥
PDB ID		2lef	2trc		1e0!	1e0 1e0	160]]e0]	1e0m	le0m	leg3
SEQ ID NO:		1598	1599		1602	1602	1602	1602	1602	1602	1602

			T	1			 r	I			т	ı
PDB annotation	ISOMERASE PINI; PEPTIDYL- PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	ISOMERASE PINI; PEPTIDYL- PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL S'- PHOSPHATE	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS	AMINOTRANSFERASE BSAT. AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS	TRANSFERASE PSAT; AMINOTRANSFERASE, PYRIDOXAL-5'-PHOSPHATE, PHOSPHOSERINE, 2 ALKALIPHILIC	LYASE ALPHA/BETA FOLD	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE
Coumpound	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	FORMIN BINDING PROTEIN; CHAIN: A;	FORMIN BINDING PROTEIN; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	CSDB PROTEIN; CHAIN: A;	SERINE HYDROXYMETHYLTRANSFER
SEQFOL D score							:	355.62				
PMF score	0.01	0.82	0.94	0.99	66'0	0.01	0.78		1.00	1.00	1.00	65.0
Verify score	-0.06	-0.19	0.72	0.25	0.25	90.0-	0.20		0.71	0.84	0.28	0.07
Psi Blast	90-99	1e-07	1.5e-09	6.8e-05	6e-05	6e-06	1.7e-67	1.7e-58	1.7e-58	5.1e-60	1.7e-61	5.1e-67
AA AA	185	125	124	121	121	148	387	389	389	389	389	387
STAR T AA	132	06	96	96	96	95	1	56	27	38	11	1
CHAI N ID	В	V.	Ą	Ą	А	В	A	А	∀	٧	Ą	А
PDB ID	1f8a	1601	1e0l	1e0m	1e0m	1f8a	1bj4	Ibjn	1bjn	15t4	lc0n	1cj0
SEQ ID NO:	1602	1603	1603	1603	1603	1603	1606	1606	1606	1606	1606	1606

	- مر،	J STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
UL N. UL		1 AA			score	score	D score		
								ASE; CHAIN: A, B;	1 CARBON METABOLISM
Idfo A			386	1.7e-67	0,11	99.0		SERINE	TRANSFERASE SHMT, SERINE
								HYDROXYMETHYLTRANSFER	METHYLASE; ALPHA PLP
*** · · · · · · · · · · · · · · · · · ·								ASE; CHAIN: A, B, C, D;	ASFAKIAIE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
leji A		1	386	1.7e-66	-0.02	0.42		SERINE	TRANSFERASE SHMT; SERINE-
								HYDROXYMETHYLTRANSFER	GLYCINE CONVERSION,
								ASE; CHAIN: A, B, C, D;	PYRIDOXAL 5'-PHOSPHATE, 2
									ASYMMETRIC DIMER
	l								
1bj4 A		-	344	3.4e-62	0.15	0.18		SERINE	TRANSFERASE TRANSFERASE,
								HYDROXYMETHYLTKANSFER ASE: CHAIN: A:	METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE
Ibjn A	ŀ	88	343	1.7e-49			282,66	PHOSPHOSERINE	AMINOTRANSFIRM
								AMINOTRANSFERASE; CHAIN:	AMINOTRANSFERASE, L-SERINE
•	,							A, B;	BIOSYNTHESIS
Ibjn A		27	337	1.7e-49	0.58	1.00		PHOSPHOSERINE	AMINOTRANSFERASE PSAT;
								AMINOTRANSFERASE; CHAIN:	AMINOTRANSFERASE, L-SERINE
\dagger								A, B;	BIOSYNTHESIS
lbt4 A		গ্ৰ	336	5.1e-51	0.59	1.00		PHOSPHOSERINE	TRANSFERASE PSAT;
								AMINOTRANSFERASE; CHAIN:	AMINOTRANSFERASE,
		_						A;	PYRIDOXAL-5'-PHOSPHATE,
\dashv						'			PHOSPHOSERINE, 2 ALKALIPHILIC
_		=	344	8.5e-56	-0.01	0.48		CSDB PROTEIN; CHAIN: A;	LYASE ALPHA/BETA FOLD
Icj0 A			344	6.8e-62	-0.04	0.43		SERINE	TRANSFERASE SHMT;
								HYDROXYMETHYLTRANSFER	HYDROXYMETHYL TRANSFERASE,
								ASE; CHAIN: A, B;	1 CARBON METABOLISM
Idfo A		m	344	5.1e-66	0.07	-0.02		SERINE	TRANSFERASE SHMT, SERINE
		-						HYDROXYMETHYLTRANSFER	METHYLASE; ALPHA PLP
								ASE; CHAIN: A, B, C, D;	ASPARTATE, AMINO
7									TRANSFERASE, (AAT)-LIKE FOLD
leji A			44	5.16-59	0.07	0.07		SERINE HVDB OXXX (ETHX) TB ANSEED	TRANSFERASE SHMT; SERINE-
								THE PROPERTY OF THE PROPERTY OF THE	OF LOINE CON VENSION,

PDB annotation	PYRIDOXAL 5-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN		LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
Coumpound	ASE; CHAIN: A, B, C, D;	STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP. 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME B12-18 KDA UBCH7; CHAIN: C;	EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;
SEQFOL D score				70.36		,	
PMF score		0.04	0.11		0.01	0.22	0.04
Verify score		-0.48	-0.33		-0.23	-0.31	0.02
Psi Blast		0.00051	1.2e-06	7.5e-05	3.4e-11	0.003	6.8e-14
END		70	82	345	603	611	8885
STAR T AA				%	552	515	828
CHAI N ID		4	K.	-		¥	∢
PDB ID		lbg1	15xk	1quti	1 chc	1fbv	1b0x
SEQ B G		1608	1608	1609	1612	1612	1614

A		CHAI	STAR TAA	END	Psi Blast	Verify	PMF	SEQFOL D score	Compound	PDB acree and
NO: 1614	164f	• 4	825	885	6.8e-15	0.21	-0.09		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDI ICTION OF IGOMER
1616	1a25	4	588	716	1.5e-26	0.08	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID
-1 14-2			-		·					BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN
1616	1a25	¥	728	864	4.5e-16	0.32	1.00		PROTEIN KINASE C (BETA); CHAIN: A. B:	CALCIUM-BINDING PROTEIN CALB;
									•	BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN
1616	1a25	A	755	871	1.5e-36	0.33	0.37		PROTEIN KINASE C (BETA);	CALCIUM-BINDING PROTEIN CALB;
									CHAIN: A, B;	CALCIUM++/PHOSPHOLIPID
										BINDING PROTEIN, 2 CALCIUM. BINDING PROTEIN
1616	1byn	Ą	588	717	3e-28	-0.05	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
1	·									SYNAPTOTAGMIN, C2-DOMAIN,
								-		EXOCYTOSIS,
-	\ <u>-</u>									NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1616	Ibyn	Ą	618	721	1.2e-08	-0.02	0.59		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
										SYNAPTOTAGMIN, C2-DOMAIN,
										EXOCYTOSIS,
										NEUROTRANSMITTER 2 RELEASE,
					,	1				ENDOCYTOSIS/EXOCYTOSIS
1616	1byn	∢	732	826	6.8e-22	0.85	0.89		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
									,	SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS
										MEI BOTT ANISMITTED 2 DEI DA SE
										ENDOCYTOSIS/EXOCYTOSIS
1616	1djx	¥	909	669	1.5e-14	-0.50	0.00		PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-D1;
			-						rhosrnolirase c, chain; A, B;	PHOSPHOMIC DIESTER HYDROLASE, HYDROLASE, LIPID

PDB annotation	DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	TRANSFERÁSE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL.SERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN			ENDOCYTOSIS/EXOCYTOSIS C2-
Coumpound		SYNAPTOTAGMIN III; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;
SEQFOL D score									
PMF score		1.00	1.00	0.99	0.17	0.58	00.1	0.59	0.36
Verify score		0.13	-0.11	0.20	0.12	60:0-	0.12	0.39	0.07
Psi Blast		8.5e-59	1.2e-27	4.5e-14	1.7e-39	9e-20	6e - 30	6.8e-22	3.4e-46
END AA	-	875	716	845	872	726	717	856	874
STAR T AA		587	588	728	751	909	288	732	730
CHAI N ID		Ą	∢	¥	¥				¥
PDB ID		1dqv	Idsy	Idsy	Idsy	lrlw	Irsy	Irsy	3rpb
SEQ ID NO:		1616	1616	1616	1616	1616	1616	1616	1616

PDB annotation	DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS		CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++PHOSPHOLIPID	BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB;	CALCIOM++/FHUSPHULIPIU	BINDING PROTEIN, 2 CALCIOM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, C2-DOMAIN,	EXOCYTOSIS,	NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, C2-DOMAIN,	EXOCYTOSIS,	NEUROTRANSMITTER 2 RELEASE,	ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, C2-DOMAIN,	EXOCYTOSIS, comment	NEUROTRANSMITTER 2 RELEASE,	ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLA2;	HYDROLASE
Coumpound			PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;		PROTEIN KINASE C (BETA);	CHAIN: A, B;		SYNAPTOTAGMIN I; CHAIN: A;				SYNAPTOTAGMIN I; CHAIN: A;					SYNAPTOTAGMIN I; CHAIN: A;					CYTOSOLIC PHOSPHOLIPASE	72, CHAIN. B, B,
SEQFOL D score						59.65									= ,			144						
PMF score			0.34	1.00					0.21				1.00					8: -			•		-0.05	
Verify			0.28	90.0					0.26				0.33					-0.05					0.13	
Psi Blast		47.4	6.8e-27	1.5e-26		1.5e-26			6.8e-23				1.7e-27					3e-28					1.7e-16	
END			351	197	,	208			343				196			·•	(198					333	
STAR T AA			230	69		69		-	122				69	_			Ş	39					230	
CHAI N ID			«	¥		¥			Ą				¥					<<				•	∢	
PDB ID			la25	1a25		1825		••••	1byn	• •			1byn					loyn					Icjy	
SEQ NO.			1617	1617		1617			1617				1617				1	1617					1617	

	I		1	T	·			· · · · · · · ·	7
PDB annotation	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN				
Coumpound	SYNAPTOTAGMIN III; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID
SEQFOL D score							69.42		
PMF score	0.39	0.13	0.70	1.00	0.58	0.07		1.00	1.00
Verify score	-0.26	0.24	-0.23	-0.11	-0.09	0.16		0.39	0.12
Psi Blast	3,4e-52	1.2e-28	3.4e-21	1.2e-27	9e-20	6.8e-23	6e- 30	1.7e-27	6e-30
END AA	356	351	203	197	207	343	200	196	198
STAR	71	232	89	69	87	221	හ	69	69
CHAI N ID	¥	A	¥	∢		•			
PDB UI	ldqv	Idsy	ldsy	ldsy	Irlw	Irsy	Irsy	्रा इस्	Insy
SEQ ID NO:	1617	1617	1617	1617	1617	1617	1617	1617	1617

		<u> </u>		-					
PDB annotation		ENDOCYTOSIS/EXOCYTOSIS C2-DOMAIN, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN; RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS		ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	,	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY 2 STRUCTURE, APLYSIA KVI.1	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2
Соитроива	BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-A; CHAIN: A;		SYNAPTOTAGMIN I; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;
SEQFOL D score				-		·			
PMF		0.45	0.96		0.17	0.13	0.16	1.00	0.65
Verify score		0.15	0.22		0,29	-0.00	0.14	0.38	0.65
Psi Blast		3.4e-27	8.5e-20		1.3e-06	0.0045	1.5e-05	5.1e-26	6.8e-05
END AA		354 4	206		366	356	366	68	104
STAR T AA	O.P.G.	236	71		264	264	264	E.	ۍ
CHAI N ID		∢	•		∢	A			Ą
EDB ID		3rpb	Згрь		ІБуп	1dsy	lrsy	1a68	lbuo
SEQ ID NO:		1617	1617		1618	1618	1618	1620	1620

PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KV1.1, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22
Coumpound		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	KV BETA2 PROTEIN; CHÁIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	KVI.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KV1.1; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score				·				53.11
PMF score		66'0	66'0	0.82	0.95	1.00	0.01	
Verify score		870	15.0	-0.10	0.38	0.55	-0.18	
Psi Blast		3.4e-25	1.5e-26	1.7e-26	1.2e-26	8.5e-29	0.003	0.003
END		68	92	101	101	700	158	212
STAR T AA		3	2	8	ι.	2		parel.
CHAI N ID	•	А	E	∀	Ą		A	А
PDB ID		1 dsx	1exb	Iqdv	111	3kvt	lcun	lcun
SEQ ID NO:		1620	1620	1620	1620	1620	1621	1621

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	PDB annotation	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN- DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY- SUBUNIT, 2 BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
	Coumpound		CYCLIN HOMOLOG; CHAIN: A;	CYCLIN H; CHAIN: NULL;	CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	CYCLIN A; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING
	SEQFOL D score								
	PMF score		0.37	0.30	0.76	0.77	0.84	0.89	0.70
ing daga mengan s	Verify score	·	0.05	0.03	0.33	0.40	0.35	01.0-	-0.01
internation of the second seco	Psi Blast		1.4e-19	1.2e-12	8.5e-42	1.7e-40	12e-19	6.8e-22	1.4e-25
	END AA		149	148	148	148	169	134	165
	STAR T AA		52	78	41	47	110	33	70
• .	CHAI N ID		Ą		м		∀	Ą	A
	PDB ID		1bu2	ljkw	Iqmz	lvin	lalh	laIh	laih
	SEQ ID NO:		1623	1623	1623	1623	1624	1624	1624

PDB annotation	PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROJEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DINA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINGERICANDUA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2
Coumpound	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	1 · S		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	-		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;
SEQFOL D score								•									58.17				•		-			î. Hê		į.				The salest con-		
PMF		0.92					0.46					0.75										0.18					0.98					0.06		
Verify score		0.35					-0.29					90.0		2								-0.00					0.08	-				0.44		
Psi Blast		3,4e-33					1.7e-41				-	3.4e-45					3.4e-45					6.8e-38					1.5e-13					1.5e-11		
END AA		169					134					165					166					93					134					165		
STAR T AA		109					33					99					89					7					107				=	135		
CHAI N ID) a	pr				ن ن					၁	-				ن			112		C	•		•		ڻ ڻ					ڻ ڻ		•
PDB ID		lmey	**	•	****		Imey					1mey	•				Imey					lmey					lmey					imey		
SEQ ON ON		1624					1624		-			1624				-	1624					1624					1624					1624		

PDB annotation	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; SS GENE, NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, SS RNA 2	GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE: NMR, TFIIIA, PROTEIN, DNA.	TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3 (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YANG 1:	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT XXI, ZRIC 2 FINGER PROTEIN DIVA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	KECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION/DNA)
Coumpound		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE; CHAIN: E, F:				YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS NITIATOR ELEMENT DNA;	CHAIN: A, B;			
SEQFOL D score			-										51.82					
PMIF score		0.12		0.25				-0.02										
Verify score		0.43	·	-0.23				0.21										
Psi Blast		Je-14		3.4e-17				1.7e-13					5.1e-28					
END AA		691		165				169					166	,				
STAR T AA		110		69				117					30					
CHAI N ID		¥		¥		-		ပ			•		C					
PDB ID		9		<u> </u>			-	pqnl					pqnI					
SEQ ID NO:		1624		1624		-		1624					1624					

SEQ ID NO:	PDB CD	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1624	pqn1	U	. 39	165	5.16-28	-0.13	0.42		YY I; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1624	2adr		110	167	3.4e-15	-0.20	0.63		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1624	2drp	∢	105	165	1e-09	0.14	0.29		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1624	2gli	∢	13	164	6.8e-25	0.03	0.10		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1624	2gli	A	9%	169	8.5e-21	0.01	0.09		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1627	158q	А	3 6	186	4.5e-19			54.14	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1627	1b8q	∢	\$9	181	4.5e-19	0.83	0.84		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1627	1be9	4	48	170	1.5e-14			52.53	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN

CHAI N ID	<u> </u>	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
	1								LOCALIZATION
∀	0	88	153	1.5e-14	0.12	0.24		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
	1	35	161	3e-22			70.34	INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
	1	29	157	3e-22	0.39	0.76		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
Ą			149	3e-19	0.55	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
¥		<i>L</i> 9	176	1.2e-20	0.47	0.37		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
∢		29	149	6e-20	1.02	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER
¥		29	149	3e-22	0.75	1.00		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
A		85	143	1.5e-15	0.05	0.17		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
A		56	143	1.7e-17	0.30	0.65		TYROSINB PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS,

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PDB annotation		HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, CHECKER, APPLIE, PTP-BAS, CHECKER, APPLIE, PTP-BAS, CHECKER, APPLIE, PTP-BAS, CHECKER, APPLIES APPLI	SFECIFICITY OF BINDING	LIPID TRANSPORT APO A-I;	LIFUFKUIEIN, LIFID I KANSPORI, CHOLESTEROL METABOLISM, 2	ATHEROSCLEROSIS, HDL, LCAT-	DESIGNED HELICAL BUNDLE	DESIGNED RELICAL BOINDEE	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MKNA; SPLICING	REGULATION, RNP DOMAIN, RNA	COMPLEX	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN I, PABP 1; RRM,	PROTEIN-KNA COMPLEX, GENE
Coumpound		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;		APOLIPOPROTEIN A-1; CHAIN:	A, B, C, U;		DHP1; CHAIN: NULL;		SXL-LETHAL PROTEIN: CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*GP*UP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*GP*UP*UP*	UP*UP*UP*UP*U). CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; KNA (5-	R(P*GP*UP*UP*GP*UP*UP*	UP*UP*UP*UP*U> CHAIN: P, Q;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN I; CHAIN: A, B, C, D,	E, F, G, H; KNA (5'-
SEQFOL D score				63.32	,								74.65					•						`			81.71		
PMF		1.00					0.01		0.78								8				1.00								
Verify score		0.92					0.12		0.78								0.91				96.0							-	
Psi Blast		4.5e-22		5.1e-07			0.0043		1.7e-16				1.5e-36			,	1.5e-36				3.4e-20						1.7e-34		
END		149		258			366		128				231				229				148			-			237		
STAR T AA		56		53			325		51		-		89				2				28					_	70	- 	
CHA1		Ą		A					A				¥				∢				₹			en file of			<		
PDB UI		3pdz		lav1			4hb1	1.	167f				167f				lb7f				lovj —						lcvj		
SEQ	ON	1627		1628			1628		1629				1629		-		1629				1629						1629		

			parameter	(· · · · · · · · · · · · · · · · · · ·		
PDB annotation	REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A)
Coumpound	R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP-3); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP;); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP;); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, O, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING
SEQFOL D score			75.65	·	52.68		
PMF score		1.00		1.00		1.00	1.00
Verify		0.89		0.71		0.41	0.36
Psi Blast		1.7e-34	le-30	1e-30	16-33	5.1e-27	le-33
END		233	218	202	212	202	206
STAR T AA		71	70	71	70	11	73
CHAI N ID		A	ш	m	[£,	Ľ.	ഥ
PDB ID		lovj	1cvj	Icvj	lcvj	lcvj	Icvj
SEQ ID NO:		1629	1629	1629	1629	1629	1629

17

	; RRM, SNE	LY(A) ; RRM, sne	LY(A) ; RRM, SNE	LY(A) ; RRM, sne	RBD,	k, RBD,
PDB annotation	IN 1, PABP 1 OMPLEX, G VA	IONRNA PC IN 1, PABP I OMPLEX, G VA	IONRNA PC IN 1, PABP 1 OMPLEX, G	IONRNA PC IN 1, PABP 1 OMPLEX, G VA	S. V. C. P. A. C. P. A. C.	SIN IS NUCLEA OTEIN AI, EIN, HNRNF SINDING, 2
PDB a	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATIONRNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	NUCLEAR PROTEIN HETEROGENEOUS MEGELAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2
	PRO'	GEN PRO' REG'	GEN BINI PRO' REG	GEN BINI PRO REG	NUC RIBC NUC RRM	NUC RIBC NUC RRM
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-A); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP* O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;	HNRNP A1; CHAIN: NULL;	HNRNP AI; CHAIN: NULL;
J.	R. E. P.	7 K 4 % A 0	7 K 7 X X Q	M. W. W. W. A. C.	全	岳
SEQFOL D score		53.52				
PMF			1:00	0.99	1.00	1.00
Verify			0,35	0.51	0.69	1.05
Psi Blast		1.4e-31	8.5e-27	1.4e-31	3.4e-25	3.4e-56
END		209	202	209	144	229
STAR T AA		70	71	22	23	65
CHAI N ID		Д	ш	¤	•	
PDB ID		levj	1cvj	levj	lha1	lhaI
SEQ ID NO:		1629	1629	1629	1629	1629

PDB annotation	RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	PETEROGENEOUS NUCLEAR	MIGITAL PROTEIN AL,	NUCLEAR PROIEIN, HINKNY, KBD,	RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN		BINDING DOMAIN		BINDING DOMAIN	OUTER MEMBRANE PROTEIN.	OSMOPOKIN; OCH EKTMEMBRANE	PROJEIN, NON-SPECIFIC PORIN,	OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	+-	53	-		POLYPYRIMIDINE TRACT BINDING	PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION	\dagger					1	XI.	
Coumpound		HNRNP A1; CHAIN: NULL;	-	-			HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN D0; CHAIN: A;	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN DO; CHAIN: A;	OMPK36; CHAIN: A, B, C;		- -		OUTER MEMBRANE PROTEIN	PHOSPHOPORIN (PHOE) 1PHO 3	POLYPYRIMIDINE TRACT.	BINDING PROTEIN; CHAIN: A;		•	RNA-BINDING PROTEIN SEX-	LETHAL PROTEIN (C.	TERMINUS, OR SECOND RNA-	BINDING DOMAIN 1SXL 3	(RBD-2), RESIDUES 199 - 294	PLUS N-TERMINAL MET) 1SXL	4 (NIMR, 17 STRUCTURES) ISXL 5	
SEQFOL D score		167.63			-																		-					
PMF							1.90	· · · · · · · · · · · · · · · · · · ·	1.00		-0.19				-0.19		0.23				0.60	}				·		
Verify score							1.26		1.29		1.27				1.08		55.0				99.0	}						, ,
Psi Blast		3.4e-56					3.4e-27		1.5e-27		1.5e-11				1.5e-11		6e-17				6e-25	;						74
END AA		230					144		145		329				324		145				150	1						150
STAR T AA		99				!	71		17	,	235		_		241		ឧ				61	<u>:</u>					•	દ્
CHAI N ID							Ą		A		₩		•				∢	-										
PDB ID		1ha1					1hd1		1hd1		losm				1pho		1qm9				lsxl							1001
SEQ ID NO:		1629					1629		1629		1629				1629		1629				1629							1620

PDB annotation		INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE PROTEIN 20MF 12	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP 1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3
Coumpound	LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score					165.44	70.15
PMF score		-0.20	1.00	1.00		
Verify score		1.23	1.05	1.18		
Psi Blast		9e-13	1e-28	5.1e-57	5.1e-57	5.1e-36
END AA		328	144	233	239	229
STAR T AA		237	25	25	64	69
CHAI N ID	•		Ą	¥	∢	A
PDB ID		2omf	2up1	2up1	2up1	38x1
SEQ ID NO:		1629	1629	1629	1629	1629

-		di miantiparaturi interna			 		
PDB amotation	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION		COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B FACTOR IIA; COAGULATION/CRYSTAL STRUCTURE/HEPARIN-BINDING SITE/ 2 HIRUDIN/THROMBIN INHIBITOR	CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN- BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN- BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA- BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
Coumpound		SEX-LETHÁL; CHAIN: A, B, C;		THROMBIN; CHÁIN: A,B,C; THROMBIN; CHAIN: D,E,F; HAEMADIN; CHAIN: 1,1,K;	HORSE PLASMA GELSOLIN; CHAIN: A, B	HORSE PLASMA GELSOLIN; CHAIN: A, B	MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;
SEQFOL D score				1.0	·	876.96	
PMF		1.00		0.98	1.00		0.95
Verify		0.88	-	0.77	0.81		0.54
Psi Blast		5.1e-36		9000	0	0	6e-06
END AA		229		84	715	715	130
STAR T AA	16, 2004	70		47	\$	<i>ب</i> ر	8
CHAI N ID		Ą		I	Ą	Æ	4
PDB ID		3sx[1e0f	1d0n	140m	lakh
SEQ ID NO:		1629		1635	 1637	1637	1641

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PDB annotation	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION		DNA-BINDING PROTEIN	
Coumpound	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	PAIRED PROTEIN; CHAIN: A, B, C, DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C, DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP 3	OCT-3; 1OCP 5 CHAIN: NULL; 1OCP 6	DNA BINDING PROTEIN OCT-I POU HOMEODOMAIN DNA- BINDING PROTEIN MUTANT WITH IPOG 3 ARG GLY SER HIS MET INSERTED AT THE N- TERMINUS AND ASP ILE IPOG 4 INSERTED AT THE C- TERMINUS (INS(RGSHM- R6),INS(I66-DI) IPOG 5 (NAR,
SEQFOL D score			,					
PMF	0.55	0.33	0.49	0.98	86'0	69.0	0.62	0.78
Verify score	0.22	-0.02	0.17	0.89	0.71	0.33	99.0	0.46
Psi Blast	7.5e-06	1.5e-05	1.5e-06	1.2e-05	9e-06	90-99	1.3e-06	3e-06
END	134	136	134	134	134	134	134	134
STAR T AA	22	26	35	26	25	83	92	8
CHAI N ID	Ą	В		Ą	В			
PDB ID	lau7	1972	1bw5	191	161	1hdp	10cp	l pog
SEQ D NO:	1641	1641	1641	1641	1641	1641	1641	1641

PDB annotation							
Coumpound	13 STRUCTURES) IPOG 6	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED 1LPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED 1LPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	LIPASE PROTEIN COFACTOR PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IPCN 4	LIPASE PROTEIN COFACTOR PORCINE PANCREATIC PROCOLIPASE B 1PCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1PCN 4	LIPASE PROTEIN COFACTOR
SEQFOL D score				50,95			56.60
PMF score		0.81	0.88		1.00	1.00	
Verify score		-0.36	-0.35		-0.36	-0.36	
Psi Blast		8e-19	3e-20	3e-20	3.2e-20	6e-22	6e-22
END AA		49	65	99	69	69	69
STAR T AA		29	29	••	83 [,]	23	2
CHAI N ID		A	A	¥ .		•	
PDB ID		11pb	11pb	Ilpb	Ipen	1pcm	1pcn
SEQ ID NO:		1653	1653	1653	1653	1653	1653

PDB annotation		COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), PHOSPHOTYROSINE 2 BINDING DOMAIN (PTB)	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3
Соитроива	TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	SHC; CHAIN: A; TRKA RECEPTOR PHOSPHOPEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;
SEQFOL D score				51.48	
PIMF		0.10	0.93		0.98
Verify score		0.17	0.21		0.34
Psi Blast		0.00075	9e-24	96-24	0.00032
END		247	247	248	260
STAR T AA		110	108	108	110
CHAI N ID		∢	«	∢	¥
PDB ID		Ishc	2mmb	2nmb	2nmb
SEQ TD NO:		1654	1654	1654	1654

PDB annotation	REGULATION	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS	PHOSPHOTRANSFERASE C-SRC,	PHOSPHORYLATION, SH2, SH3, 2	PHOSPHOTYROSINE, PROTO-	ONCOGENE,	COMPLEX (SIGNAL	TRANSDUCTION/PEPTIDE)	COMPLEX (SIGNAL	TRANSDUCTION/PEPTIDE), SH3						
Coumpound		EIF1; CHAIN: NULL;	EIF1; CHAIN: NULL;	N-ETHYLMALEIMIDE. SENSITIVE FUSION PROTEIN; CHAIN: A;	HEAT SHOCK PROTEIN HSLU; CHAIN: A;	TYROSINE-PROTEIN KINASE				GRB2: CHAIN: A: SOS-1:	CHAIN: B;	٠:		SIGNAL TRANSDUCTION	PROTEIN GROWIN FACTOR RECEPTOR BOTTON 2	(GRB2, N-TERMINAL 1GBR 3	SH3 DOMAIN) COMPLEXED	WITH SOS-A PEPTIDE IGBR 4	thing 27 circost court 1 certs 5
SEQFOL D score		141.21	-																
PMF score			1.00	0.36	0.13	0.45				0.17				0.59					
Verify score			0.42	-0.15	-0.14	-0.13				0.09				60.0					
Psi Blast		1.6e-44	1.6e-44	1.6e-11	1.3e-17	4.8e-22				9.6e-15				1.6e-15					
END AA		149	149	257	260	426				386				392					
STAR T AA		29	42	186	140	334				335				335					
CHAI N ID	•			A	¥					A				Ą					
PDB ID		2if1	21.0	nggu	1g41	重				1gbc		_		1gbr					
SEQ ID NO:		1658	1658	1660	1660	1663				1663				1663					

	PDB annotation		SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14	COMPLEX (KINASE/PEPTIDE)	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, ISEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR, ISEM 19	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-
	Coumpound	ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	P56—LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE- RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	ABL TYROSINE KINASE; CHAIN: NULL;	KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO- ONCOGENE PROTEIN; CHAIN; C, D, E, F;	BETA-CATENIN; CHAIN: NULL;
े सम्बद्धिक स्थापिकी १४ (८) है। अपन्यक्षिक स्थापिकी १८ (८) है। अपन्यक्षित स्थापिकी १८ (८)	SEQFOL D score		,	***************************************					
	PMF	0.83	0.35	0.28	60.0	0.96	-0.06	0.41	0.10
Miles a disk in the	Verify score	0.40	-0.64	0.30	0.20	0.43	0.03	0.09	0.02
	Psi Blast	6.4e-15	6.4e-16	1.4e-18	1.6e-21	1.6e-16	4.8e-16	3e-05	7.5e-10
	END	389	389	425	426	389	426	416	530
	STAR T AA	333	304	334	333	330	327	36	107
•	CEAI N ID		¥	Æ	∢	¥		4	
	PDB	1 2 3	læ!	llck	lącf	Isem	2abi		2bct
	SEQ US	1663	1663	1663	1663	1663	1663	1669	1669

PDB aunotation	CATENIN, STRUCTURAL PROTEIN	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, PPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEIN'RNA) COMPLEX (NUCLEAR PROTEIN'RNA), RNA, SNRNP RIBONICI FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCL FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICI, EOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONICI FORDOTFILE	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
Coumpound		RIBONUCLBASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HARPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B'; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score								
PMF score		0.27	1.00	0.40	0.74	0.37	0.34	0.82
Verify score		0.16	0.54	0.10	0.36	0.41	-0.03	0.28
Psi Blast		6.4e-12	1.5e-37	1.5e-19	9.6e-07	1e-23	1.5e-22	9e-20
END AA		362	314	301	131	121	230	301
STAR T AA		27	23	126	27	30	53	126
CHAI N D		4	¥	Ą	A	Ą	V	4
PDB ID		la4y	la4y	la9n	la9n	la9n	la9n	1a9n
SE SE SE SE SE SE SE SE SE SE SE SE SE S		1671	1671	1671	1671	1671	1671	1671

WO 02/070539 PCT/US02/05095

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PDB annotation		COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICI, FOPROTEN	COMPLEX (NUCLEAR PROTEIN'RNA) COMPLEX (NUCLEAR PROTEIN'RNA), RNA, SYRNP RIRONI (CI EOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICI, FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIGONI (CI. POPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONICI FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH
Coumpound		U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R: U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;
SEQFOL	D score			;				,			
PMF	score	0.60	0.00	0.95	0.84	0.01	0.57	0.94	0.93	1.00	-0.19
Verify	score	0.50	0.13	0.24	0.40	0.44	0.16	0.70	0.18	0.31	0.04
Psi Blast		4.5e-24	0.00064	9e-18	9.6e-07	96-24	6e-23	1.6e-23	1.6e-21	6e-14	8e-21
END	¥¥	299	342	334	131	174	240	290	381	106	521
STAR	TAA	171	216	220	27	30	53	138	173	29	360
CHAI	e z	ပ	၁	၁	၁	သ	ပ	A •	¥	¥	A
PDB	e	la9n	la9n	1a9n	la9n	1a9n	la9n	140b	140b	1d0b	140b
SEQ	e ö	1671	1671	1671	1671	1671	1671	1671	1671	1291	1671

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PDB annotation	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N.	SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL	STRUCTURE, RAB	GEKANYLGEKANYLIKANSFEKASE,	CODAYI METHIONINE AT BITA	SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL	STRUCTURE, RAB	GEKANYLGEKANYLIKANSFEKASE,	LOR 2 RESOLUTION, N-	FORM YLMEI'HIONINE, ALPHA		TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA
Coumpound		DITBRNALIN B; CHAIN: A;	INTBRNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	RASE BETA SUBUNIT; CHAIN:	В, D;	RAB	GERANYLGERANYLTRANSFE	KASE ALPHA SUBUNIT;	GER ANYI GER ANYI TO ANCHO	RASE BETA SUBUNIT; CHAIN:	B, D;	RAB	GERANYLGERANYLTRANSFE	KASE ALFRA SUBUNII;	CED ANIM OFF ANIM TO ANION	CERAN LUERAN ILI KANSFE RASE BETA SUBINIT: CHAIN:	B, D;	RAB	GERANYLGERANYLTRANSFE	KASE ALPHA SUBUNIT;	CHAIN: A, C; KAB GERANYLGERANYLTRANSFE
SEQFOL D score															÷									
PIMF score		1.00	1.00	1.00					0.36						1.00				,		0.89		-	
Verify score		0.74	0.61	0.49					0.18						0.66						0.68			
Psi Blast		1.3e-27	8e-28	4.8e-14					3.2e-06						4.8e-10						4.8e-12			
END		196	242	250					107						130						154			
STAR T AA		43	70	145											27						48			
CHAI N ID		Y	Ą	∢ '			-	•	∢		_				⊀						∢			
PDB ID		1405	1406	1 dce					ldce						dce					,	ldce			
SEQ ID NO:		1671	1671	1671					1671					1	1671						1671			

PDB annotation	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE. RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2	CONTRACTILE PROTEIN LEUCINE.	RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CONTRA A CTR E DE CTERA I ELICIARE	RICH REPEAT RETA-RETA-AI PHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	SIGNALING PROTEIN	PHOTORECEPTOR, G PROTEIN-	COUPLED RECEPTOR, MEMBRANE	PROTEIN, 2 RETINAL PROTEIN,	VISUAL PIGMENT	RNA BINDING PROTEIN TAP (NFX1);	RIBONUCLEOPROTEIN (RNP, RBD	OR RRM) AND LEUCINE-RICH-	REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1);	RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH-
Coumpound	RASE BETA SUBUNIT; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN:	₩;	OUTER ARM DYNEIN; CHAIN:	£		OUTER ARM DYNEIN; CHAIN:	A;		OTTED ADM DENEM: CHAM:	OUTEN ANIM DINEIN, CITAIN.	(RHODOPSIN; CHAIN: A, B					NUCLEAR RNA EXPORT	FACTOR 1; CHAIN: A, B;			NUCLEAR RNA EXPORT	FACTOR 1; CHAIN: A, B;
SEQFOL D score				•.						,												~~~			
PMF		0.11	69'0		0.01			0.64			0.50	70.5			0.05					0.72				0.22	
Verify		-0.03	-0.14		-0.32			0.03			000	6.0			-0.04					0.27				-0.08	
Psi Blast		1.6e-13	1.4e-21	•	6.4e-10			1.6e-12			3 20 1K				1.5e-14					%e- 05				1.1e-05	·
END		289	299		08£			148			105	22			702					83				107	
STAR		154	165		201			27			80	3			403					27				55	
CHAI N ID		4	A		¥			¥			4	¢			Э					∀				4	
PDB		6sp1	lds9	·	6sp1			1ds9			0.61	Cen :			8 8 J1					I fol				1fol	
SEQ NO.		1671	1671		1671			1671			1671	5			1671					1671				1671	

	PDB annotation	REPEAT 2 (LRR) RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRK, LEUGINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, MEROHEDRAL TWINNING, MEROHEDRAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN 1.1GA SE	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3,
	Coumpound	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D:	CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45;
्रकारो अस्ट्रिक्ट्राक्ट्राक्ट्रान्ट । राज्यात्म्यक्ट्राक्ट्राक्ट्राक्ट्रान्ट (स्ट. क्ट. १५ क्ट्रुक्ट्राक्ट्रिक्ट्राप्ट रोज्या रहे ।	SEQFOL D score							
	PMF score	0.90	0.25	0.68	0.21	1.00	0.34	0.59
Z. a I William a reported to	Verify score	0.32	0.0	0.41	0.19	0.33	-0.85	-0.62
	Psi Blast	1.1e-05	1.5e-16	6e-50	1.4e-16	3e-31	1.6e-08	1.3e-08
	END AA	107	154	314	424	334	129	129
	STAR T AA	45	53	29	30	83	90	92
•	CHAI	æ	¥				Ą	*
	EG EG EG	1fo1	1 yrg	2bnh	2bnh	2bnh	ISI .	181
	SEQ B Sign	1671	1421	1671	1671	1671	1673	1673

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PDB annotation	UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN LIGASE	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE	TRANSFERASE ALLOSTERY,	COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE	ANTIFUNGAL PROTEIN OSMOTIN- LIKE PROTEIN; ANTIFUNGAL PROTEIN, PATHOGENESIS- RELATED PROTEIN, PR-5D, 2 OSMOTIN, THAUMATIN-LIKE	PROTEIN	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE
Coumpound	CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;		GLYCEROL KINASE; CHAIN: O, Y, Z, X;	GLYCEROL KINASE; CHAIN: O,	Y, Z, X;	PR-5D; CHAIN: NULL;		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A
SEQFOL D score					310.87		52.19					
PMF		0.28		1.00					0.09	0.00	-0.14	-0.18
Verify score		-0.51		0.56					-0.16	1.29	1.60	0.79
Psi Blast		6.4e-09		0	0		0.009		4.5e-17	6e-16	6e-15	3e-19
END AA		162		491	492		161		201	162	118	197
STAR T AA		06		18	18		 -		134	42	4	28
CHAI N ID		∢		0	0				A	∢	Ą	А
PDB UD		1fs2		1bu6	1bu6		laun		1c2a	1c2a	1c2a	1c2a
SEQ NO:		1673		1675	1675	-	1676		1676	1676	1676	1676

PDB annotation	INHIBITOR	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOL OGOUS HEVEIN-LIKE DOMAINS	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERA VITIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SIPPER ANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN SACCHARIDE	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA;
Coumpound		AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A:	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A:	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A:	AGGLUTININ ISOLECTIN VVAGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VIAGGLUTININ ISOLECTIN V; CHAIN: A:	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN
SEQFOL D score												
PMF score		0.01	-0.14	-0.12	-0.18	-0.12	0.15	-0.14	-0.17	-0.14	-0.12	0.15
Verify score		0.87	1,43	1.28	1.17	0.05	1.32	1.70	1.37	0.98	1.34	1.29
Psi Blast		1.2e-17	1.2e-19	3e-18	1.5e-18	1.3e-14	7.5e-18	1.5e-19	3e-18	Ie-18	3e-17	1.1e-16
END		192	100	172	116	761	98	142	172	192	106	986
STAR T AA		104	10	22	10	124	3	2	77	104	10	3
CHAI N ID		∢	₹	¥	Ą	¥	Ą	¥	¥	∢	• ∀	A
PDB ID		Iehd	lehd	pyel	leis	leis	leis	leis	leis	len2	len2	len2
SEQ NO:		1676	1676	1676	1676	1676	1676	1676	1676	1676	1676	1676

PMF SEQFOL score D score
59.75
24 67
50.00
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PDB annotation	BINDING, HYDROLASE, 3 GLYCOPROTEIN	MEMBRANE ADHESION SHORT	CONSENSUS REPEAT, SUSHI,	COMPLEMENT CONTROL PROTEIN,	2 N-GLYCOSYLATION, MULTI-	DOMAIN, MEMBRANE ADHESION	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITION	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS		
Соитроии		HUMAN BETA2-	GLYCOPROTEIN I; CHAIN: A;				ANTISTASIN; CHAIN: NULE;						ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;		-				MEMBRANE PROTEIN	VITELLINE MEMBRANE
SEQFOL D score											-														66.09							
PMF score		-0.20			•		-0.15	•					0.29						-0.12						-						-0.20	
Verify score		0.83					0.92						1.27						0.53				,								1.30	
Psi Blast		1.4e-30					6e-15						1.1e-15						6e-21					-	6e-21						I.5e-14	
END AA		200					168						175						198						202						107	
STAR T AA		3					13						74		-				63						33					ad House		
CHAI N ID		Ą		•						•							-											_			¥	
PDB ID		1qub	*****				Iskz						lskz						lskz						1skz		<u>-</u>				1мпо	-
SEQ ID NO:		1676					1676						9/91						1676						1676						9291	

WO 02/070539 PCT/US02/05095

PDB annotation				OXIDOREDUCTASE ALPHA-BETA- ALPHA MOTIF, FLAVIN	CONTAINING PROTEIN, OXIDASE	FLAVOENZYME FLAVOENZYME,	OXIDOREDUCTASE	OXIDOREDUCTASE ADR, NADPH:	AUKENODOMINA OVIDOBEDITOTA SE:	FLAVOENZYME, MAD ANALYSIS,	ELECTRON TRANSFERASE	OXIDOREDUCTASE TETRAHEME	FLAVOCYTOCHROME C	FUMARATE REDUCTASE, 2	OXIDOREDUCTASE	OXIDOREDUCTASE IRON-SULFUR	FLAVOPROTEIN, ELECTRON	TRANSFER, OXIDOREDUCTASE	OXIDOREDUCTASE IRON-SULFUR	FLAVOPROTEIN, ELECTRON	TRANSFER, OXIDOREDUCTASE	OXIDOREDUCTASE LIPOAMIDE	DEHYDROGENASE, L PROTEIN, E3,	DLDH, DIHYDROLIPOAMIDE	DEHYDROGENASE, MULTIENZYME	COMPLEX 2 PROTEIN, PYRUVATE	DEHYDROGENASE COMPLEX,	GLYCINE 3 DECARBOXYLASE COMPLEX, FLAVOPROTEIN
Coumpound		1VMO 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	D-AMINO ACID OXIDASE; CHAIN: A;		L-ASPARTATE OXIDASE;	(C. 1101)	ADRENODOXIN REDUCTASE;	CRAIN A,			FLAVOCYTOCHROME C	FUMARATE REDUCTASE;	CHAIN: A;		TRIMETHYLAMINE	DEHYDROGENASE; CHAIN: A,	B	TRIMETHYLAMINE	DEHYDROGENASE; CHAIN: A,	B,	DIHYDROLIPOAMIDE	DEHYDROGENASE; CHAIN: A,	B, C, D;				
SEOFOL	D score		101.83	,			• •	62.05								·												
PMF	score			0.19		0.13	· ·			•		0.36				0.12			0.70			0.00			***			
Verify	score		3 A (\$14)	-0.46		-0.05						-0.03				-0.09			-0.08			-0.41	,					
Psi Blast	•		4.5e-23	0.00048		0.00014		3.2e-37				3.2e-09				1.6e-12			9e-13	•		0.003						
END	AA		189	68		46		457				318				182			329			118						
STAR	TAA		8	11	•	L		10				142				2			\$			2						
CHAI	N ID		• V	ĸ		A		A				¥				A	-		Ą			Ą						
PDB	Ð		9wga	dQo1		1chu	,	lcje				1d4d			-	1djn			ldjn			ldxl						
SEO	Α̈́		1676	1680		1680		1680				1680				1680			1680			1680						

Parker material back

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PDB annotation	OXIDOREDUCTASE LIPOAMIDE DEHYDROGENASE, L PROTEIN, B3, DLDH, DIHYDROLIPOAMIDE DEHYDROGENASE, MULTIENZYME COMPLEX 2 PROTEIN, PYRUVATE DEHYDROGENASE COMPLEX, GLYCINE 3 DECARBOXYLASE COMPLEX FLAVOPROTEIN	COMPLEX (OXIDOREDUCTASE/TRANSFERASE) E3BD; REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE	OXDOREDUCTASE FLAVOENZYME, OXIDASE, ENANTIOMERIC SPECIFICITY, O- 2 AMINOBENZOATE, ACTIVE SITE FUNNEL, HELICAL DOMAIN, FAD- 3 BINDING DOMAIN			OXIDOREDUCTASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE, FLAVOPROTEIN, FAD, NADP	OXIDOREDUCTASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE,
Counipound	DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B, C, D;	DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B; DIHYDROLIPOAMIDE ACETYLTRANSFERASE; CHAIN: C:	L-AMINO ACID OXIDASE; CHAIN: A, B, C, D, E, F, G, H;	ELECTRON TRANSPORT(FLAVOCYTOCHR OME) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCSD) 1FCD 3	ELECTRON TRANSPORT(FLAVOCYTOCHR OME) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCSD) IFCD 3	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;
SEQFOL D score		e.		= <u></u>	8 5.√.√		
PMF	0.39	0.69	0.04	0.22		0.51	-0.01
Verify score	-0.07	-0.04	-0.50	0.10		0.11	0.00
Psi Blast	3.2e-94	1.6e-95	1.6e-07	1.6e-19	1.6e-19	7.5e-05	1.6e-74
END	462	462	49	407	394	118	459
STAR T AA	∞	14	9	10	6	2	8
CHAI N ID	¥	Ą	A	¥	¥	A	4
PDB ID	اطّ <i>ما</i>	1ebd	1f8s	1 fcd	lfed	1fec	Ifec
SEQ ID NO:	1680	1680	1680	1680	1680	1680	1680

PDB annotation	FLAVOPROTEIN, FAD, NADP	FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE, OXIDOREDIJCTASE	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE		
Coumpound		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D, P;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE DIHYDROLPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LPF 3 FLAVIN-ADENINE- DINUCLEOTIDE (FAD) 11.PF 4	OXIDOREDUCTASE
SEQFOL D score						
PMF score		0.05	0.37	0.05	0.15	0.04
Verify score		-0.79	-0.74	-0.56	-0.25	-0.14
Psi Blast		0.00032	3.2e-06	0.00032	3.2e-95	3.2e-75
END AA		43	43	391	462	462
STAR T AA		22	12	310	∞	13
CHAI N ID		K	A	∢	∢	
PDB U		1 foh	1 fum	1 fum	llpf	11vI
SEQ B SO:		1680	1680	1680	1680	0891

PDB annotation			OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 FLAVOPROTEIN FAD PAK	OXIDOREDUCTASE OXIDOREDUCTASE, OXIDOREDITCTASE, NAD	OXIDOREDUCTASE OXIDOREDUCTASE		TRANSCRIPTION INHIBITOR BETA-PROPELLER	TRANSCRIPTION INHIBITIOR BETA-PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBLINIT:
Coumpound	DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LVL 3 NICOTINAMIDE-ADENINE- DINUCLEOTIDE (NAD+) 1LVL 4	OXIDOREDUCTASE (H202(A)) NADH PEROXIDASE (NPX) (E.C.1.11.1.1) MUTANT WITH CYS 42 INHP 3 REPLACED BY A1.4 (C42A) INHP 4	SURFACE PROTEIN; CHAIN: NULL;	L-ALANINE DEHYDROGENASE; CHAIN: A;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A. D:	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-AIPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B: GT-GAMMA:
SEQFOL D score		76.88							
PMF score			0.22	0.11	90.0	0.35	10.0	66.0	-0.14
Verify score			-0.06	0.02	-0.43	-0.06	0.25	0.56	0.43
Psi Blast		1.6e-57	6.4e-88	0.0048	6.4e-05	3.2e-91	1.6e-61	3.2e-72	1,4e-55
END AA		418	463	<i>LL</i> 1	49	462	479	624	476
STAR T AA		12	9	145	4	80	173	304	155
CHAI N ID				¥	¥	A.	A	Ą	В
PDB ID		lnhp	lojt	1pjc	1908	3lad	lerj	lerj	1got
SEQ ID NO:		1680	1680	1680	1680	1680	1681	1681	1681

		·	·				
PDB annotation	GAMMAI, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNA1, TRANSDUCER), G	COMPLEX (GTP-BINDING/TRANSDUCER.) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER.), G PROTEIN, HETEROTRIMER.2 SIGNAL TRANSDUCTION		OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN; 2 BETA-BARREL, TRANSMEMBRANE	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	
Coumpound	CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;		OMPK36; CHAIN: A, B, C;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3
SEQFOL D score		74.60					
PMF score			0.71		-0.20	-0.18	-0.20
Verify score			0.76		0.86	1,11	0.90
Psi Blast		1.4e-55	3.2e-74		4.5e-10	1.5e-12	1.2e-11
END AA		524	621		52	100	80
STAR T AA		179	302		n	œ	4
CHAI N ID		B	m	,	⊄	∢	
PDB ID		1got	1got		HISO I	losm	1pho
SEQ D NO:		1681 .	1681	, ,	0801	1685	1685

PDB engement	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE PROTEIN 20MF 12	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN		CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOI DING, A TPA SE	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOLDING, A TPASE	CHAPERONIN HSP60 CLASS, ATP, MAGNESIUM, CHAPERONIN	TRANSFERASE PYRUVATE KINASE, GLYCOLYTIC ENZYME, HOMOTETRAMER, 2 TRANSFERASE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA, RINDING
Id	INTEGRAL MEMBI PORIN MATRIX PO PORIN; 20MF 7 PO PROTEIN 20MF 12	STRUCTURAL PROTEIN REPEATS OF SPECTRIN, HELICAL LINKER REGIO TANDEM 3-HELIX COIL. STRUCTURAL PROTEIN		CHAPERONIN THERMOPI ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC PROTEIN FOI DING A TRA	CHAPERONIN THERMOPI ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC	CHAPERONIN MAGNESIUM	TRANSFERASE PYRUVA GLYCOLYTIC ENZYME, HOMOTETRAMER, 2 TR.	COMPLEX (Z) COMPLEX (Z) ZINC FINGER
Coumpound	MATRIX FORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	ALPHA SPECTRIN; CHAIN: A, B, C;	HYDROLASE CYTIDINE DEAMINASE (CDA) (E.C.3.5.4.5) COMPLEXED WITH ICTT 3 3,4- DIHYDROZEBULARINE (DHZ) ICTT 4	THERMOSOME; CHAIN: A, B;	THERMOSOME; CHAIN: A, B;	GROEL; CHAIN: A, B, C, D, E, F, G. H. I. J. K. L. M. N:	PYRUVATE KINÁSE; CHAIN: A, B, C, D, E, F, H, G;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONICI EOTTIDE BINDING
SEQFOL D score								·
PMF	-0.19	0.04	0.22	1.00	1.00	0.72	0.23	-0.19
Verify score	1.14	-0.05	-0.02	-0.12	-0.29	-0.14	-0.18	0.06
Psi Blast	1.3e-10	0.00015	9.6e-27	8e-55	6.4e-51	1.6e-68	0.0008	1.4e-09
END AA	08	210	124	186	186	186	106	114
STAR T AA	∞	86	14	15	20	12	2	33
CHAI N ID		A		V	æ	Ą	Ą	¥
PDB ID	2omf	Icun	lett	1a6d	1a6d	1der	1pk1	laih
SEQ ID NO:	1685	1688	1690	1692	1692	1692	1692	1696

PDB annotation	PROTEIN	COMPLEX (ZINC FINGER,DNA) COMPLEX (ZINC FINGER,DNA), ZINC FINGER, DNA-BINDING PROTFIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (SINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE, NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
Coumpound	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN; C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRETION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score				·		Englis E September Contract	
PMF		-0.14	-0.18	-0.17	-0.12	-0.19	-0.14
Verify score		0.07	0.07	0.10	0.16	0.08	0.04
Psi Blast		6.4e-27	3.2e-19	8e-35	1.1e-09	1,4e-13	3.2e-28
END AA		168	114	142	114	38	168
STAR T AA		06	31	61	87	69	63
CHAI N ID		4	ပ	O	Ð	A	ပ
80g CI		lalh	lmey	lmey	Imey	1 11 3	lubd
SEQ No.		1696	9691	1696	9691	1696	1696

PDB annotation	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONTICI FOPROTFIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), KNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL	ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA SUBUNIT. BETA SUBUNIT		TRANSFERASE CRESTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	FORMYLMETHIONINE, ALPHA
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R: U2 A; CHAIN: A. C: U2 B".	CHAIN: B, D;	INTERNALIN B; CHAIN: A;		RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE RASE BETA SUBUNIT: CHAIN:	B, D,	RAB	GERANYLGERANYLTRANSFE	KASE ALPHA SUBUNIT;	GERANYLGERANYLTRANSFE
SEQFOL D score																		
PMF score		-0.11	9.0¢	0.00		96'0		1.00		0.1					00'1			
Verify score		0.03	0.03	-0.34	ï	0,29	•	0.51		0.68					0.22			
Psi Blast		4.8e-17	6.46-13	6e-11		6.4e-13.		1.4e-28		3.2e-15					3.2e-17			
END		144	115	140		115		140		4					137			
STAR T AA		7		43		∞ 0		81		4					39			
CHAI N ID		Ą	¥	Ą		ပ		A	-	∢					∀	•	•	
PDB ID		2gli	la9n	1a9n		1a9n		140b		age I					1dce			
SEQ No:	W 100	1696	1698	1698		1698		1698	900.	1098					1698			

PDB annotation	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	TRANSCRIPTION RNA 1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA 1P, RANGAP, LRR, LEUCINE- 2 RICH REPEAT	PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS.	ENDOCYTOSIS/EXOCYTOSIS SUPERHELIX OF HELICES	ENDOCYTOSIS/EXOCYTOSIS SUPERHELIX OF HELICES	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA	BNA BRIDING BROTTER/BNA TBA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	GENE REGULATION/RNA POLY(A)
Coumpound	RASE BETA SUBUNIT; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN: A;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	TARGET OF MYBI; CHAIN: A, B;	TARGET OF MYB1; CHAIN: A, B;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*	OP*UP*UP*UP*U)- CHAIN: P, Q;	A, B; RNA (5'-	R(P*GP*UP*UP*UP*UP*UP*UP* I IP*I IP*I IP*I IP*I IP*I IP*I IP*I	POLYDENYLATE BINDING
SEQFOL D score			: :										
PIMF		0.24	0.21		0.49	1.00	0.1	-0.06		201	2		-0.15
Verify score	i	-0.55	-0.36	٠.	0.06	0.84	0.78	000		900	0 ()		0.05
Psi Blast		8e-23	3e-09		9.6e-10	1.4e-44	1.2e-56	1.4e-22		6 40 20	000	-	3.2e-31
END AA		142	133		139	141	143	268		104	ř		307.
STAR T AA		25				2	2	126		330	9 7 7		128
CHA1 N ID		Ą	ď			• •	¥	A	_	<	¢		A
PDB CI		1ds9	lyrg		Zbnh	leik	lelk	1b7f		11,96	7		1cvj
SEQ NO:		1698	1698		1698	1699	1699	1700		1700	3		1700

PDB annotation			GENE REGULATION/RNA POLY(A) RINDING PROTEIN 1 PARP 1: RRM	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN I, PABP I; KRM,	BEGIN ATTONIANA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN I, PABP I; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			RNA BINDING PROTEIN RNA-	MANA DESCRIPTION OF STREET	BINDING DOMAIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RIBONUCLEOPROTEIN UIAII7;	RIBONUCLEOPROTEIN, RNP	DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING	DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1,
Coumpound		O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1: CHAIN: A. B. C. D.	E, F, G, H, RNA (5-	R(*AP*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN I; CHAIN: A, B, C, D,	D/* A D*	AP*AP*AP*A)-3'; CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A); CHAIN: M, N,	O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	THE ANGROPIA C. OTTABLE A.	no an ilden C; Chain: A;	HU ANTIGEN C; CHAIN: A;		UI SMALL NUCLEAR	RIBONUCLEOPROTEIN A;	CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;		,	HNRNP A1; CHAIN: NULL;	
SEQFOL D score																															
PIMF			0.64					0.07					1.00						0.71	500		0.00		0.58			0.37			-0.17	
Verify			0,46					0.27					0.72						0.30	50.0	6,73	0.55		0.71			0.82			0.26	
Psi Blast			4.8e-25					6.4e-26					3e-21						3.2e-22	1 (1.13	1.06-17	3.2e-16		3e-17		_ ;	1.5e-16			4.8e-31	
END			216					233					461						208	905	<u>}</u>	209		417			412			301	
STAR T AA	,_		128					128					331						126	202	34/	127		323			321			126	
CHAI		•	Ľ.					щ					н						Ą	-	¢	¥					Ą				
PDB			lcvj					1cvj					lcvj						1d8z	1402	70n1	1d9a		1tht			1fjc			1ha1	
SEQ	NO:		1700					1700					1700			,			1700	1700	3	1700		1700			-1700			1700	

PDB annotation	NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	NUCLEAR PROTEIN HINRY RED	RRM, RNP, RNA BINDING, 2 RIBONIICI EOPROTEIN	RNA BINDING PROTEIN RNA.	BINDING DOMAIN		RNA BINDING PROTEIN RNA- BINDING DOMAIN										;	
Coumpound		HNRNP AI; CHAIN: NULL;			HNRNP A1; CHAIN: NULL;				HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN DO;	CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO;	CHAIN: A;	RIBONUCLEOPROTEIN	PROTEIN FROM UI SMALL	RIBONUCLEOPROTEIN (SNRNP	UI) INRC 3 (N-TERMINAL	FRAGMENT, RESIDUES 1 - 95)	MUIANI WITH GLN 85 INKC 4	REPLACED BY CYS (Q85C) INRC 5	RIBONUCLEOPROTEIN	PROTEIN FROM UI SMALL	RIBONUCLEOPROTEIN (SNRNP
SEQFOL D score			-	,												· [].	ight Bh						
PMF		-0.19			66'0				0.77			86.0		0.49							0.43		
Verify score		0.17			0.78				0.82			0.86		-0.09	_						-0.19		_
Psi Blast		1.6e-20			1.4e-34				4.8e-23			1.3e-20		1.6e-12							1.3e-12		-
END		405			481				206			399		503			_				207		
STAR TAA		226			325				127			331		127							127		
CHAI N ID									¥	-		∢		∢							В	-	
PDB ID	- , <u>u - , u</u> e	1ha1			Ihai				1hd1			Ihd1		Inrc							Inrc		
SEQ ID NO:		1700			1700				1700			1700		1700							1700		

PDB annotation			RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION		COMPLEX (RIBONUCLEOPROTEIN/RNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN,
Coumpound	.	UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POLYPYRIMIDINE TRACT. BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	U1A SPLICEOSOMAL PROTEIN; IURN 5 CHAIN: A, B, C; IURN 6 RNA 21MER HAIRPIN (5'- (AP*AP*UP*CP*CP*AP*UP*UP* IURN 11 CHAIN: P, Q, R IURN 13	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A;
SEQFOL	D Score								
PMF	score		-0.14	0.33	0.99	0.10	0.11	0.84	96.0
Verify	a score		0.25	0.06	0.71	0.59	0.47	0.82	09:0
Psi Blast			4.8e-09	1.46-15	6e-16	3.2e-18	I.3e-20	1.16-17	4.5e-16
END	¥		217	211	406	206	210	411	406
STAR	4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.		128	126	323	127	126	328	322
CHAI	3		¥		₹	Ą			•
PDB	3		1qm9	lsxI	Iurn	Zmss	2sxl	2sxl	2ula
SEQ	ğ		1700	1700	1700	1700	1700	1700	1700

PDB annotation	NUCLEAR PROTEIN	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEINDNA) HNRNP AI, UPI; COMPLEX (RIBONUCLEOPROTEINDNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROFESTATI	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION
Coumpound	CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;	TUMOR SUPPRESSOR PIGINK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA;
SEQFOL D score							67.76	
PMF score		0.05	-0.19	-0.14	0.87	1.00		1.00
Verify		0.53	0.01	0.35	0.49	1.01		0.92
Psi Blast		9.6e-13	1.1e-34	4.8e-22	1.3e-35	3.2e-29	4.5e-30	3e-45
END		206	311	410	484	474	191	298
STAR T AA		127	126	226	325	329	35	145
CHAI N ID		A	A	Ą	¥	₹		В
PDB ID		ZnZf	2up1	2up1	Zup1	38X	1aSe	1awc
SEQ ID NO:		1700	1700	1700	1700	1700	1701	1701

PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGIT ATTOMONA) CARBAI BHA	GABPBETAI; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA BRIDING, 2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	CTB ANSCRIPTION TO THE ANSCRIPTI	TIMENSCRIPTION	KEGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN ETS DOMAIN	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABFBEIAI; COMPLEX	(IKANSCKIPIJON	AFGULATION/DNA), DNA-BINDING,	ANKYRIN REPEATS	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETAI; COMPLEX
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA; CHAIN: A: GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	INCIENT BEIN I; CHAIN; B;	ייייי כווחוי ה' ה'				GA BINDING PROTEIN ALPHA;	DECTAIN: A; GA BINDING	DNA: CHARL D. E.	ים יח אוואניס ישוח				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;
SEQFOL D score																	• '			· ·			90.41		
PMF				1.8					1.00			-				8.					,				
Verify score				0.94					06.0							===									
Psi Blast				1.1e-40				_	3e-39					7		1.06-37							3e-45		
END AA				298					165						,,,	201							363		
STAR T AA				120					15						17	-							212		
CHAI N ID				20,				•	æ						P	Δ							2 0,	,	
PDB ID				lawc					lawc		· · · · · ·				+	18WC				- , -		7	lawc		1
SEQ ID NO:				107					1701						1701	1			-,_	_			10/1		

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PDB annotation	(TRANSCRIPTIONICS) REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TO ANSCRIPTION 2 EACTOR	COMPLEX (TRANSCRIPTION S FACTOR COMPLEX (TRANSCRIPTION GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION BEGULATION DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA!; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA!; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING
Coumpound	DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score			· .		
PMF		1.00	1.00	1.00	1.00
Verify score		0.64	0.25	1.07	0.46
Psi Blast		1.2e-41	3.26-32	16-32	66-39
END AA		395	427	405	199
STAR T AA		212	250	278	45
CHAI N ID	•	Д	щ	щ	æ
EDB ID		lawc	lawc	lawc	lawc
SEQ ID NO:		1701	1701	1701	1701

	PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANK YRIN REPEATS, TRANSCRIPTION 3 PACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,						
	Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI 9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
	SEQFOL D score				87.58		·				
	PMF score		1.00	1.00		1.00	1.00	0.77	1.00	1.00	1.00
ne (i Definishing) karan n	Verify		0.72	0.42		0.85	0.81	0.39	0.67	0.44	0.80
	Psi Blast		4.8e-37	3e-37	1.4e-38	7.5e-38	1.5e-37	1.4e-38	4.5e-30	1.4e-36	1.4e-38
	END AA		661	_	301						234
	STAR T AA		20	113	145	17	183	215	279	46	82
•	CHAI		М							_	
	PDB ID	-	lawc	15d8	1bd8	15d8	1bd8	15d8	15d8	15d8	1bd8
	SEQ El Si		1701	1701	1701	1701	1701	1701	1701	1701	1701

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PDB annotation	ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT KINASE CELL CYCLE 2 CONTROL	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN CYCL REDEFENDENT
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	B;			CYCLIN-DEPENDENT KINASE 6. CHAIN: A. BIONIX AD: CHAIN:	B;			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	Ď.				CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	Ä				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;	•			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score					0000	80.38																						
PIME		9.1								1.00			•			00'1					1.00						1.00	
Verify score		0.72								0.92						0.48					0.43						0.32	
Psi Blast		9e-38			00	1.56-39			i	1.5e-39						1.4e-38					3e-39						9e-38	
END		271			485	0/1				170						338					401						205	
STAR T AA		41			5	71				13						183					215						46	
CHAI N ID		മ				Δ.				В						ca ca					Д						മ	
FD8		iplx			161.	XIQ1			i	1blx						16lx					16lx						16lx	
SEQ D NO:		1701			1201	7				1701						1701					1701						1701	

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PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONF/GROWTH PACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITIOR,	CYCLIN-2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN.	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	TRANSCRIPTION FACTOR P65;	PSOD; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;	-			NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-
SEQFOL D score	ļ			92.05											14. 19. 19. 19.		89.22											
PMF		0.25						1.00		1.00		0.93										0.35				9.1		
Verify score		0.24						0.60		0.80		0.43										0.19				0.71		
Psi Blast		3.2e-30		1.3e-35	-			3e-37		1.5e-36		1.4e-29					9e-38					1.2e-53				1.5e-39		
END AA		432		177				237		40]		431					236					371				173		
STAR T AA		253		6				104		269		253					20					145				17		
CHAI N ID		∀		Ą				¥		¥		⊀					∢.					<u> </u>				Ω		
PDB UD		1bu9		1bu9				1695		s6PI		lihb					liho			•		E E				ž.		
SEQ No: D	,	1701		1701				1701		1701		1701					1701					1701				1701		

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SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ë	e	a Z	TAA	¥		score	score	D score		
									B-ALPHA; CHAIN: D;	
1701	likn	Ω	212	427	1.1e-38	0.05	0.92		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
									CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN; C; I-KAPPA- B-ALPHA; CHAIN; D;	IKB/NFKB COMPLEX
1701	likn	Ω	215	403	3e-50	0.49	660		NF-KAPPA-B P65 SUBUNIT:	TRANSCRIPTION FACTOR P65:
					_				CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	IKB/NFKB COMPLEX
1701	lika	a	45	232	4.8e-43	0.11	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
			-						CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
					,				SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	IKB/NFKB COMPLEX
1701	likn	0	45	240	4.5e-52	0.13	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
-			•						CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
1701	lika	Ω	45	253	4.5e-52			81.35	NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
					•				CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
						- "			B-ALPHA; CHAIN: D;	
10/1	ikn	Ω	82	276	4.5e-52	0.28	0.99		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
									CHAIN: A; NF-KAPPA-B P50D	PSOD; TRANSCRIPTION FACTOR,
						4 de la composição de l			SUBUNIT; CHAIN; C; I-KAPPA- B-ALPHA; CHAIN; D;	IKB/NFKB COMPLEX
1701	Imyo		247	391	1.5e-30	0.26	0.71		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
										ACETYLATION, NMR, ANK-REPEAT
1701	Infi	ш	113	311	9e-51	0.58	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
					•				NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
					,				I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									Ť.	REGULATION/ANK REPEAT),
1701	Ju1	B	143	401	3e-49	0.10	0.99		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX

PDB annotation	(TRANSCRIPTION REGULATION/ANK REPEAT) ANKYRIN 2 REPEAT TRAILX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION PEGII ATTOMANK REPEAT)	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION REGILLATION/ANK REPEAT)	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REGANK REPEAT) COMPLEX	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(I'RANSCRIPTION	REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ANKYRIN REPEATS, CELL-CYCLE	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
Commpound	J-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, E.	F ₂	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	I.KAPPA-B-ALPHA; CHAIN: E, F.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D; LKAPPA-B-AI PHA: CHAIN: E			NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ė.	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,			REGULATORY PROTEIN SWI6;	CHAIN: A, B;		REGULATORY PROTEIN SWI6;	CHAIN: A, B;
SEQFOL D score							87.55																70.20	
PMF		1.00	, —	0.70							1.00				1.00					0.28				
Verify score		0.94		0.42					,		0.50				0.59					-0.06				
Psi Blast		4.5e-39		1.1e-38			1.5e-51				1.5e-51				6.4e-43					4.5e-36			4.5e-36	
END		170	•	427	,		242				238				232					287			320	
STAR T AA		17	,	210			42				43		_		44					61			76	
CHAI N ID		ਦ		E			ш				13				ш		-			₽'			∀	
PDB TD		lnfi		Infi			lnfi				lnfi				lnfi					1sw6			1sw6	-
SEQ No.		1701		1201			1701				1701				1701					1701			1701	:

	PDB annotation	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN		PROTEIN KINASE CDK2; PROTEIN
	Coumpound	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;	CALCTUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	TRANSFERASE (PHOSPHOTRA NSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	CYCLIN-DEPENDENT PROTEIN
And majories (freder) displikation (freder) to pulgidate frederical to considerate de de se	SEQFOL D score	70.78				
	PMF score	72	0.55	0.65	0.86	0.11
रेका महिन्दीर्विकार क्रिकेट	Verify score	* \$1150 f f f	-0.07	0.08	0.30	0.22
Typical and and a	Psi Blast	7.5e-35	4.5e-37	1.6e-70	6.4e-98	1.le-46
	END AA	396	283	303	312	266
	STAR T AA	214	81	31	29	29
•	CHAI N ID	ш	ф	·	ш	
	PDB ID	lycs	1ycs	1a06	lapm	laq1
	SEQ TO NO:	1701	1701	1702	1702	1702

PDB annotation	KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION. MITOSIS, INHIBITION	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT			TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2
Coumpound	KINASE 2; CHAIN: NULL;	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	IMPORTIN ALPHA; CHAIN: A;
SEQFOL D score							ji ta r	
PMF score		1.00	1.00	0.75	0.86	0.98	0.60	0.24
Verify score		0.22	0.29	0.10	10:0	0.35	0.26	0.26
Psi Blast		0.0003	1.4e-33	3.2e-99	8e-94	3.2e-49	4.8e-49	6e-05
END		416	260	312	303	264	266	551
STAR T AA		231	278	29	29	53	29	328
CHAI		¥	ď	म	ក	U ·		¥
PDB ID		163u	1b3u	lcmk	Ісф	1£3m	Thei	lial
SEQ No.		1702	1702	1702	1702	1702	1702	1702

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PDB annotation	ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA- CATENIN, STRUCTURAL PROTEIN	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCUIM-BINDING PROTEIN	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL
Coumpound		TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	PHOSPHORYLASE KINASE; CHAIN: NULL;	CALMODULM; CHAIN: A; RS20; CHAIN: B;	BETA-CATENIN; CHAIN: NULL;	RECOVERIN; CHAIN: NULL;	CYCLIN HOMOLOG; CHAIN: A;
SEQFOL D score			-	81.88					
PMF score		0.75	96.0		0.99	0.09	0.52	0.07	0:30
Verify		0.30	0.51		0.48	-0.18	-0.31	-0.04	-0.26
Psi Blast		1.3e-58	8e-57	3.2e-42	6.4e-71	1.18-19	0.0001	0.0003	3.2e-26
END		304	265	334	264	453	560	440	352
STAR T AA		29	29	m	31	301	438	308	157
CHAI N ID			¥			V	•		4
PDB ID		1koa	1kob	1p38	1phk	lvrk	2bct	liku	1bu2
SEQ ID	Ö	1702	1702	1702	1702	1702	1702	1704	1705

PDB annotation	CYCLIN	TRANSCRIPTION/DNA TRANSCRIPTION INITIATION FACTOR IIB, TFIIBC; TATA-BOX	FACIOR, 1A1A SECUENCE- BINDING PROTEIN, PROTEIN-DNA COMPLEX, CYCLIN-LIKE FOLD,	HELIX-TURN-HELIX, 2 TATA-BOX, TRANSCRIPTION/DNA		COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN-	DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE	COMPLEX (PROTEIN	KINASE/CYCLIN), CYCLIN, CDK, 2	PHOSPHORYLATION, SUBSTRATE COMPLEX	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-	SUBUNIT, 2 BINDING PROTEIN	TRANSCRIPTION INHIBITOR BETA- PROPELLER		COMPLEX (GTP-BINDING/TRANSDUCER) BETA1,	TRANSDUCIN BETA SUBUNIT;	GAMMAI, IRANSDUCIN GAMMA	SUBDING, COMPLEA (O. 17- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2
Coumpound		GENERAL TRANSCRIPTION FACTOR IIB; CHAIN: A, E, I, M, Q; TATA BOX BINDING C, TATA BOX BINDING	PROTEIN; CHAIN: B, F, J, N, K; ADMLP TATA-BOX DNA CONTAINING IIB	RECOGNITION CHAIN: C, G, K, O, S; ADMLP TATA-BOX DNA CONTAINING IIB	RECOGNITION CHAIN: D, H, L, P, T;	CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C;	G2/MITOTIC-SPECIFIC CYCLIN A. CHAIN: B. D. SUBSTRATE	PEPTIDE; CHAIN: E, F;			CYCLIN A; CHAIN: NULL;		TRANSCRIPTIONAL	B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-	BETA; CHAIN: B; GT-GAMMA;	CHAIN: G;	
SEQFOL D score			-											-			-	
PMF score		0.17				0.01					0.04		1.00		0.93			
Verify score		-0.02				-0.21					-0.11		0.65		0.35			
Psi Blast		1.3e-23				4.8e-49					4.8e-48		8e-67		1.4e-59			
END		350				345					345		571		529			
STAR T AA		183				136					142		27.7		230			
CHAI N ID		Ą				æ			•				A		В			
PDB ID		1c9b				1qmz					1vin		lerj		lgot			
SEQ NO.		1705				1705					1705		1708		1708			

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PDB annotation	SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT;	GAMMAI, TRANSDUCIN GAMMA SUBUNIT, COMPLEX (GTP- BINDING/TRANSDUCEB), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT;	GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDINGTRANSDUCER), G	PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (TRANSFERASE/PEPTIDE)	(TRANSFERASE/PEPTIDE)			n na			COMPLEX (PROTO- ONCOGENE/EARLY PROTEIN) SRC	HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION,
Coumpound		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA;	CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA;	CHAIN: G;		C-SRC TYROSINE KINASE; CHAIN: A, B, ACE-FORMYL	PHOSPHOT I R-GLO-(M,N-) DIPENTYL AMINE); CHAIN: C, D;	TRANSFERASE(PHOSPHOTRA	ONCOGENE TYROSINE	KINASE (E.C.2.7.1.112) 1AB2 3	(SRC HOMOLOGY 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4	(NMR, 20 STRUCTURES) 1AB2 5	FYN PROTEIN-TYROSINE KINASE; CHAIN: F;	PHOSPHOTYROSYL PEPTIDE; CHAIN: P
SEQFOL D score		104.96													
PMF score				1.00			60.0		0.12					90.0	
Verify score				0.55			0.56		0.38					0.47	
Psi Błast		1.6e-69		1.6e-69			8e-25		1.6e-22					4.8e-21	
END		569		695	**************************************		380		382	·				378	
STAR T AA		242		280			282		282					282	
CHAI N ID		В	•	Д			Y							দ	
PDB ID		1got		1got	2		1a09		lab2					laot	
SEQ EQ		1708		1708			1709		1709					1709	

	PDB annotation	PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PHOSPHOTRANSFERASE, COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES	COMPLEX (KINASE/PEPTIDE)	COMPLEX (TYROSINE KINASE/PEPTIDE)
	Сонтроинд		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	P56LCK TYROSINE KINASE; CHAIN: L; PHOSPHONOPEPTIDE CHAIN: P;	GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	P56—LCK— TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO) YQPQPA; ILCK 14 CHAIN: B; ILCK 15	HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN; A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU- ILE; ILKK 11 CHAIN; B; ILKK
	SEQFOL D score								
A SAME AND A STANDARD	PMF score	-	0.01	0.07	-0.01	0.07	0.16	0.01	0.15
i kugun kang menteberah kanal Kangun kang menteberah kanal	Verify score		0.29	0.31	0.44	0.13	0.18	80.0	0.49
And the second	Psi Blast		1.6e-24	1.6e-22	1.1e-17	1.4e-19	1.1e-17	6.4e-26	3.2e-21
·	END		385	379	379	375	377	379	379
	STAR T AA		284	275	281	286	281	242	282
	CHAI N#D				A	ا ا		¥	¥
	PDB		15kI	161	losy	lcwd	1 Ifns	11ck	1 <u>K</u>
	S e S		1709	1709	1709	1709	1709	1709	1709

								The second secon
PDB annotation				TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN	TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSFERASE	HAI OPEROXIDASE	HALOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE, OXIDOREDUCTASE	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE,
Coumpound	12	PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	SIGNALLING PROTEIN PHOSPHATIDYLINOSITOL 3- KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4	SHP-2; CHAIN: A, B;	HCK SH2; CHAIN: NULL;	CHI OR OPER OYID A SE 1	CHAIN: A, B, C,	CHLOROPEROXIDASE L; CHAIN: A, B, C;
SEQFOL D score						85.12	\$0 \$4 \$4 \$4 \$4	
PMF score		0.07	0.78	0.04	0.25		. · · · · · · · · · · · · · · · · · · ·	1.00
Verify score		0.51	0.33	-0.31	0.19			0.36
Psi Blast		1.6e-24	6.4e-18	3.2e-27	1.6e-22	30.41		3e-41
END		380 380	383	439	379	357	}	356
STAR T AA		284	286	257	281	76	2	84
CHAI N ID		4		Ą		V		Ą
PDB ID		1sha	2pna	2shp	3hck	1200		1a88
SEQ NO:		1709	1709	1709	1709	1710		1710

PDB annotation	ASE	ASE	DASE A1,	ASE A1;	ASE,	4SE	1SE	ASE F.	T. C.	OXIDOREDIICTASE PROPIONATE		ASE	ASE F;	ASE,	OXIDOREDUCTASE, PROPIONATE		SE	SE, PROLINE	E. SERINE	NTHOMONAS		DROLASE,	HALOALKANE DEHALOGENASE,	YDROLASE	DROLASE,	HALOALKANE DEHALOGENASE,	YDROLASE	SE	C. C	IDASE A2;	SE.	OXIDOREDUCTASE, PEROXIDASE,	ALPHA/BETA 2 HYDROLASE FOLD,	
PDB	OXIDOREDUCTASE	HALOPEROXIDASE	CHLOROPEROXIDASE A1,	HALOPEROXIDASE A1;	HALOPEROXIDASE,	OXIDOREDUCTASE	HALOPEROXIDASE	HALOPEROXIDASE F.	HALOPEROXIDASE	OXIDOREDICT	COMPLEX	HALOPEROXIDASE	HALOPEROXIDASE F;	HALOPEROXIDASE,	OXIDOREDUCT.	COMPLEX	AMINOPEPTIDASE	AMINOPEPTIDASE, PROLINE	IMINOPEPTIDASE, SERINE	PROTEASE, 2 XANTHOMONAS	CAMPESTRIS	HYDROLASE HYDROLASE	HALOALKANEI	ALPHA/BETA-HYDROLASE	HYDROLASE HYDROLASE	HALOALKANEI	ALPHA/BETA-HYDROLASE	HALOPEROXIDASE	HALOPEROXIDAGE	CHLOROPEROXIDASE A2;	HALOPEROXIDASE,	OXIDOREDUCTA	ALPHA/BETA 2 I	MULAINI MISSI
Coumpound		BROMOPEROXIDASE A1;	CHAIN: NULL;				CHLOROPEROXIDASE F;	CHAIN: NULL;				CHLOROPEROXIDASE F;	CHAIN: NULL;			•	PROLINE IMINOPEPTIDASE;	CHAIN: A, B;				HALOALKANE	DEHALOGENASE; CHAIN:	NULL;	HALOALKANE	DEHALOGENASE; CHAIN:	NULL;	BROMOPEROXIDASE A2;	CHAIN; NULL;					
SEQFOL D score		95.47					83.84										67.83			-	i	94.11						98'68			•			-
PIMF score												1.00	,												1.00	•				-				
Verify score												0.61	•												0.45			-						
Psi Blast		8e-31					9e-4]					9e-41	-				1.5e-36					3e-43			3e-43			8e-32		**** <u>*</u>				
END AA		360					357					356					355					357			356			357						
STAR T AA		78				ļ	78					2					63					4			23			%						
CHAI N ID																	₹														•			
PDB ID		1889				,	la8s			***		1a8s				1	Jazw		_			1b6g					1	Ħ						
SEQ ID NO:		1710					1710					1710					1710					17.10		2,1	07/1			1710						

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HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE 1-S BOND	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA- HYDROLASE	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CISTARCOE, HYDROLASE	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HALOGENASE; CHAIN: A; DEHALOGENASE; CHAIN: A;	TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	EPOXIDE HYDROLASE; CHAIN: A, B;
77.34	122.01	. ,				119.90	
		1.00	1.00	0.63	0.07		1.00
		0.58	0.60	0.11	0.25		0.52
3.2e-36	75-96	9e-47	3e-44	3e-13	4.8e-09	9.6e-37	8e-43
357	360	358	358	661	212	356	356
72	67	74	73	101	26	99	62
Ą	Ą	.A	¥		•	∢	¥
Ic4x	lcqw	lcqw	Icv2	lcvl	lcvl	1ehy	lek1
1710	1710	1710	1710	1710	1710	1710	1710
	A 72 357 3.2e-36 77.34 2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4-DIENOATE CHAIN: A;	1c4x A 72 357 3.2e-36 77.34 2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4-DIENOATE CHAIN: A; CHAIN: A; 1cqw A 67 360 9e-47 122.01 HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	1c4x A 72 357 3.2e-36 77.34 2-HYDROXY-6-OXO-6-PHENOATE 1cqw A 67 360 9e-47 122.01 HALOALKANE 1cqw A 74 358 9e-47 0.58 1.00 HALOALKANE 1cqw A 74 358 9e-47 0.58 1.00 HALOALKANE DEHALOGENASE; 1-CHOROHEXANE CHAIN: A; CHLOROHEXANE CHAIN: A; CHLOROHEXANE CHAIN: A;	1c4x A 72 357 3.2e-36 77.34 2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A; 1cqw A 67 360 9e-47 122.01 HALOALKANE DEHALOGENASE; 1-CHLOROHEXANE CHAIN: A; 1cqw A 74 358 9e-47 0.58 1.00 HALOALKANE DEHALOGENASE; 1-CHLOROHEXANE CHAIN: A; 1cv2 A 73 358 3e-44 0.60 1.00 HALOALKANE DEHALOGENASE; CHAIN: A;	1c4x A 72 357 3.2e-36 77.34 2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE 1cqw A 67 360 9e-47 122.01 HALOALKANE 1cqw A 74 358 9e-47 0.58 1.00 HALOALKANE 1cv2 A 73 358 3e-44 0.60 1.00 HALOALKANE 1cv2 A 73 358 3e-44 0.60 1.00 HALOALKANE 1cv1 73 358 3e-44 0.60 1.00 HALOALKANE 1cv2 A 73 358 3e-44 0.60 1.00 HALOALKANE 1cv1 101 199 3e-13 0.10 HALOALKANE DEHALOGENASE; CHAIN: A; 1cv1 101 199 3e-13 0.11 0.63 TRIACYLGLYGEROL HYDROLASE; CHAIN: NULL; HYDROLASE; CHAIN: NULL; HYDROLASE; CHAIN: NULL; HYDROLASE; CHAIN: NULL;	1c4x A 72 357 3.2e-36 77.34 2-HYDROXY-6-OXO-6-DENOATE 1cqw A 67 360 9e-47 122.01 HALOALKANE 1cqw A 74 358 9e-47 0.58 1.00 HALOALKANE 1cv2 A 73 358 3e-47 0.58 1.00 HALOALKANE 1cv1 101 199 3e-13 0.11 0.60 HALOALKANE 1cv1 101 199 3e-13 0.11 0.60 HALOALKANE 1cv1 101 199 3e-13 0.11 0.60 HALOALKANE 1cv1 101 199 3e-13 0.11 0.63 HALOALKANE 1cv1 101 199 3e-13 0.11 0.63 HALOALKANE 1cv1 97 212 4.8e-09 0.25 0.07 HYDROLASE; CHAIN: NULL; HYDROLASE; CHAIN: NULL; HYDROLASE; CHAIN: NULL; HYDROLASE; CHAIN: NULL;	164x A 72 357 326-36 77.34 PHENYLHEXA-Z-A-DIENOATE 1cqw A 67 360 9e-47 122.01 HALOALKANE 1cqw A 74 358 9e-47 0.58 1.00 DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A; 1cv2 A 73 358 3e-44 0.60 1.00 DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A; 1cv2 A 73 358 3e-44 0.60 1.00 DEHALOGENASE; CHAIN: A; 1cv1 A 66 356 9.6e-37 119.90 SOLUBLE EPOXIDE 1cqw A 77 212 4.8e-09 0.25 0.07 TRIACYLGLYCEROL 1chy A 66 356 9.6e-37 119.90 SOLUBLE EPOXIDE 1cqw A 77 212 4.8e-09 0.25 0.07 HYDROLASE; CHAIN: NULL; 1chy A 66 356 9.6e-37 119.90 SOLUBLE EPOXIDE 15 D; D; D; D; D; D; D; D

PDB annotation	N: HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISH BSTITHTED TREA 2 NHIBITOR	 	-	┼	 	HYDROLASE PSEUDOMONADACEAE, CIS- PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE,	 HYDROLASE PSEUDOMONADACEAE, CIS- PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID	N: EPOXIDE HYDROLASE EH; EPOXIDE HYDROLASE ALPHABETA HYDROLASE	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT
Coumpound	EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: A, B;	LIPASE, GASTRIC; CHAIN; A. B.	PARA-NITROBENZYL ESTERASE; CHAIN: A;	TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	EPOXIDE HYDROLASE; CHAIN: A, B;	PROLYL AMINOPEPTIDASE; CHAIN: A;	TRIACYL-GLYCEROL- HYDROLASE; CHAIN: D, E;
SEQFOL D score									80.11	
PMF	1.00	1.00	1.00	0.07	0.27	0.81	0.28	1.00		0.11
Verify score	0.56	0.58	69.0	0.13	0.76	0.38	0.37	0.46		0.10
Psi Blast	1.2e-54	8e-43	3e-56	1.5e-06	4.5e-05	6e-25	4.8e-09	1.5e-45	6.4e-29	4.8e-10
END	356	356	356	226	215	238	212	358	360	215
STAR T AA	07	62	69	98	85	8	97	47	<i>L</i> 9	64
CHAI	A	В	м	Ą	• V	Q	Д	¥	A	Q
PDB ID	lek1	lek1	1ek1	1hlg	1qe3] dge	14ge	1907	Iqtr	4lip
SEQ U	1710	1710	1710	1710	1710	1710	1710	1710	1710	1710

PDB annotation	ANALOGUE, ENANTIOSELECTIVITY			METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN I; RAGI, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER
Coumpound		VIRUS EQUINE HERPES VIRUS. 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	RAGI; CHAIN: NÜLL;	RAGI; CHAIN: NULL;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;
SEQFOL D score								
PMF		0.84	0.71	0.00	0.74	0.64	0.12	0.88
Verify score		-0.31	-0.18	-0.64	-0.02	-0.00	0,16	0.52
Psi Blast		6e-17	3.2e-14	4.5e-14	36-11	1.3e-07	0.009	1.4e-28
END AA		328	332	321	328	331	297	307
STAR T AA		275	278	276	272	280	194	171
CHAI N ID	•			Ą			A	Ą
PDB ID		1chc	Ichc	1g25	Irmd	1rmd	lorz	lerj
SEQ ID NO:		1711	1711	1711	1711	17	1712	1712

PDB annotation	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP-BINDING/TRANSDUCER) BETA!, TRANSDUCIN BETA SUBUNIT; GAMMA!, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL, TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA!, TRANSDUCIN BETA SUBUNIT; GAMMA!, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCIS 14 NMA SCHII	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE,
Coumpound	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GF- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMIMA; CHAIN: G;	MJ0882; CHAIN: A;	CATECHOL O- METHYL TRANSFERASE; CHAIN: NULL;
SEQFOL D score			63.92			
PMF	0.96	1.00		1:00	0.43	0.30
Verify score	0.33	0.43		0.54	-0.10	-0.07
Psi Blast	1.3e-44	6.4e-39	1.6e-48	1.6e-48	6.4e-10	7.5e-11
END	289	290	307	305	446	455
STAR T AA	37	14	1	28	338	334
CHAI N ID	٧	В	В	Ф	A	
PDB ID	lerj	1got	lgot	1got	1dus	lvid
SEQ ID NO:	1712	1712	1712	1712	1713	1713

PDB annotation	METHYL TRANSFERASE, NEUROTRANSMITTER DEGRADATION		REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	HYDROLASE HEPATITIS C VIRUS, BIFUNCTIONAL, PROTEASE- HELICASE	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	GENE REGULATION APO PROTEIN	GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF44, HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACEOREM IFFA, IFFA, HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC
Coumpound			DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	PROTEASE/HELICASE NS3; CHAIN: A, B;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EXCINICLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIÁTION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR
SEQFOL D score													
PMF score		-	0.53	96.0	0.77	0.62	0.86	0.99	0.43	0.18	0.35	-0.06	0.21
Verify score			0.14	0.50	0.42	0.09	-0.11	0.35	0.20	0.07	0.02	0.04	90.0
Psi Blast	·		3.2e-13	4.5e-16	0.0006	3.2e-13	1.5e-16	3e-20	3.2e-18	1.1e-39	1.6e-25	0	1.6e-25
END			497	494	170	497	513	525	208	508	691	508	169
STAR T AA			345	371	50	345	370	346	354	338	7	119	2
CHAI N ID			A	Ą	A	¥	A	Æ	Ą	¥	¥	æ	В
PDB ID			1040	1640	1cu1	1d2m	1d2m	1 d9 x	1 d9 x	1fuk	1fuu	1fuu	1fuu
SEQ No:			1719	1719	1719	1719	1719	1719	1719	1719	1719	1719	1719

33923 23

PDB annotation	INITIATION FACTOR 44; IF4A, HELICASE, DEAD-BOX PROTEIN	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE	GENE REGULATION EIF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY	HYDROLASE/DNA ATP-DEPENDENT HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA: HELICASE PCRA	HYDROLASE, DNA, PRODUCT COMPLEX		INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN	COLLAGEN-BINDING COLLAGEN- BINDING, HEMOGRACIO, DIMITO FOTIDE BINDING FOI D	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN	CONNECTIN 471, CONNECTIN; ITTIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN
Coumpound	4A; CHAIN: A, B;	HCV HELICASE; CHAIN: A, B;	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	HELICASE PCRA; CHAIN: A, F; HELICASE PCRA; CHAIN: B, G; DNA (S) DA TEXTEXTEX TEXTEX 30.	D(A(5'-C), II II II II II II II)), CHAIN: C, D; DNA (5'-D(*GP*C)- 3'); CHAIN: H; DNA (5'- D(*AP*CP*TP*GP*C)-3');	CIDIN: 1;	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	VON WILLEBRAND FACTOR; CHAIN: A, B;	AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	TITIN; CHAIN; NULL;	TITIN; CHAIN: NULL;
SEQFOL D score				·				75.90	89.44	65.12	-		
PMF score		0.22	0.39	0.33			1.00		-		0.99	-0.01	0.41
Verify score		0.29	0.10	0.22			0.62				0.79	0.22	0.65
Psi Blast		0.0014	3,26-23	9000.0			1.1e-21	1.1e-21	4.8e-17	1.6e-26	1.6e-26	3.2e-11	9e-12
END AA		170	169	82			170	220	213	221	220	302	427
STAR T AA		13	2	2			28	28	31	23	30	211	329
CHAI N ID		Ą	Ą	Ą	,		Ą	Ą	Ą	•			
PDB ID		1hei	Iqde	2pjr			laox	laox	latz	Iauq	lauq	1bpv	1bpv
SEQ ID NO:		1719	1719	1719			1721	1721	1721	1721	1721	1721	1721

P	PDB CHAI	I STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
_					score	score	D score		
1									TYPE III
آگ	1bpv	342	418	3.2e-13	0.47	0.09		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
. هـ	16qu A	337	419	3.2e-12	0.45	0.48		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1cfb	e	208	427	1.4e-11			52.60	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGILAN	
	•			•				(CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO	a di sa
								AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES	
				ļ				610 - 814)) 1CFB 5	
Ictb		209	4 2	1.46-11	60.0	-0.07		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN	
		······································						(CHYMOTR YPTIC FRAGMENT	
								AMINO PROXIMAL	
								FIBRONECTIN TYPE III	
								610 - 814)) ICFB 5	
Ick4	4 4	33	170 201	9.6e-21	0.46	00'1		INTEGRIN ALPHA-I; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, A DHE SLOW
lck4	4 A	*	209	6e-38	96.0	1.00		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN,
1fna	80	338	415	1.1e-13	0.49	0.72		CELL ADHESION PROTEIN	AURESION
							,		

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Commonnel	DDR opportation
ΑÖ	<u>n</u>	OI N	TAA	¥¥		score	score	D score		
						•			FIBRONECTIN CELL- ADHESION MODULE TYPE III- 10 1FNA 3	
1721	1fnf		106	444	1.4e-26	-0.05	0.13		FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	CELL ADHESION PROTEIN RED, EXTRACELLIFAR MATRIX 15NF 18
1721	1fmf	•	27	415	1.6e-31	-0.00	-0.06		FIBRONECTIN; 1FNF 6 CHAIN:	CELL ADHESION PROTEIN RGD, EXTRACEL LILLAR MATRIX 1500 150
1721	1fnf		28	425	1.6e-31			91.50	FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACEL III AP MATRIX IENE 19
1721	1fnh	Ą	107	421	1.6e-24	0.16	-0.09		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1721	1fnh	≺	133	421	1.1e-26			73.33	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1721	1fnih	Æ.	213	445	1.1e-26	-0.04	0.49		FIBRONECTIN; CHAIN; A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1721	1fins	⋖	30	217	1.6e-25	76.0	1.00		IMMUNOGLOBULIN NMC-4	IMMUNE SYSTEM VON
									IMMUNOGLOBULIN NMC-4	WILLEBRAIND FACTOR, GLYCOPROTEIN IBA (A:ALPHA)
									IGGI; CHAIN: H; VON	BINDING, 2 COMPLEX
					т Эм⊖⊅				CHAIN: A;	(WILLEBRAND/IMMINUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B
1721	lido		32	208	758-37			01.05	MITTER CRIME CHARLES NOW .	VON WILLEBRAND DISEASE
			}	3	ξ.,	-		21:03	IN IEGKIN; CHAIN: NOLL;	CELL ADHESION PROTEIN A. DOMAIN INTEGRIN CELL
						-				ADHESION PROTEIN,
					•					GLYCOPROTEIN, EXTRACELLULAR
1721	lido		34	206	7.5e-37	0.65	1.00		INTEGRIN: CHAIN: NITI.	CELL ADHESTON PROTEIN A.
				-				to considerate		DOMAIN INTEGRIN, CELL
								e e e e e e e e e e e e e e e e e e e		ADHESION PROTEIN,
										GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX CYTOSKEI FTON
1721	11fa	¥	33	213	1.5e-36			78.17	CD11A; 1LFA 5 CHAIN: A, B; 1LFA 6	CELL ADHESION LFA-1, ALPHA- L'BETA-2 INTEGRIN, A-DOMAIN:

PDB annotation	ILFA 8	CELL ADHESION LFA-1, ALPHA- L',BETA-2 INTEGRIN, A-DOMAIN; ILFA 8	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION INTEGRIN, CELL ADHESION	CELL ADHESION INTEGRIN, CELL ADHESION	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRUX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
Commpound		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	TENASCIN; CHAIN: A, B;
SEQFOL D score			75.51						
PMF score		1.00		0.58	0.37	1.00	1.00	-0.07	0.72
Verify score		89:0		0.08	0.42	0.55	0.99	0.05	9.04
Psi Blast		1.5e-36	6.4e-24	6.4e-24	8e-17	8e-21	7.5e-28	1.6e-18	1.6e-22
END		209	425	415	445	170	209	419	421
STAR T AA		34	211	215	342	30	34	214	214
CHAI N ID		¥				¥	¥ ·	¥	Ą
PDB ID		11ffa	Imfin	1mfn	1mfn	1905	lqc5	1qg3	lqr4
SEQ ID NO:		1721	1721	1721	1721	1721	1721	1721	1721

PDB annotation	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRIICTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRICTI IN A 1 PROTEIN				PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	COAGULATION FACTOR	-
Coumpound	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR. 36 STR ICTURES) 1TTF 3	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NIJ.1. 2HFT 5	HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS
SEQFOL D score	77.31								
PMF score		0.34	0.99	0.81	0.70	0.84	0.86	-0.17	-0.19
Verify		0.55	0.06	0.92	0.27	0.55	12.0	0.08	0.08
Psi Blast	1.6e-22	1.4e-13	3e-12	1.2e-13	3.2e-14	1.3e-06	3.2e-11	1.1e-12	1.5e-16
END AA	421	445	301	421	415	281	421	416	422
STAR T AA	214	337	210	335	337	215	337	215	215
CHAI N ID	A	∢				¥	₹		EL C
PDB ID	1qr4	1qr4	Iten .	Iten	J#1	2fnb		2hft	3hhr
SEQ ID NO:	1721	1721	1721	1721	1751	1721	1721	1721	1721

PDB annotation		TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN	KINASE KINĀSE, SIGNAL TRANSDUCTION,	CALCIUM/CALMODULIN					-										D				COMPLEX (KINASE/INHIBITOR)
Coumpound	RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE;	CHAIN: NULL;	TRANSFERASE(PHOSPHOTRA NSFERASE) \$C-/AMP\$-	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATAL YTIC SUBUNIT) ALPHA	ISOENZYME MUTANT WITH	SER 139 1APM 4 REPLACED BY	ALA (/SI39AS) COMPLEX WITH	INHIBITOR PKI(5-24) AND THE	DETERGENT MEGA-8 1APM 6	TRANSFERASE(PHOSPHOTRA	NSFERASE) &C-/AMP\$-	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3	(CATALY IIC SUBUNIT) ALPHA	ISOENZYME MUTANT WITH	SEK 139 IAPM 4 KEPLACED BY	ALA (/S139A\$) COMPLEX WITH	THE PEPTIDE IAPM S	INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 LADM 6	CYCLIN-DEPENDENT KINASE
SEQFOL D score										-			59.46				,	. '					52.92
PMF score		0.58	0.27		0.88																		
Verify score		0.19	-0.31		-0.22																		
Psi Blast		4.5e-06	4.8e-39		3.2e-47				•				3.2e-47										8e-24
END AA		236	355		356								413										355
STAR T AA		146	147		143								11		-								104
CHAI N ID		В			<u>г</u>								ш							•	,		A
PDB		lfun	1a06		1apm								lapm										1bi8
SEQ No:		1723	1724		1724							1 437	1724				-		440.40				1724

PDB annotation	CDK6; P19INK4D; CYCLIN DEPENDENT KINASB, CYCLIN DEPENDENT KINASB INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX					TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
Coumpound	6; CHAIN: A, C; CYCLIN: DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (B.C.2.7.1.37) 1CMK 4	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	SERNE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D:	P38 MAP KINASE; CHAIN: NULL;
SEQFOL D score			59.27		58.35		56.49
PMF score		0.70		0.77		0.54	,
Verify score		-0.22		-0.14		0.07	
Psi Blast		1.6e-48	1.6e-48	1.6e-48	1.6e-48	4.8e-36	1.le-18
END		356	413	356	399	361	401
STAR T AA	·	143	69	143	77	147	77
CHAI N ID		កា	Ш	Œ	Э •	C	
PDB ID		Icmk	lcmk	Ictp	Iotp	113m	lian
SEQ NO:		1724	1724	1724	1724	1724	1724

PDB annotation	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGILLATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2928	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINETTHEONINE-PROTEIN, 2 KINASE, ATP-BINDING,	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	AMINE/CARBOXYLATE LIGASE AMINE/CARBOXYLATE LIGASE	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX NUCLEAR PROTEIN/RNA), RNA, SWRNP PROMICT ROPP OTERN	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING
Coumpound	TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	PHOSPHORYLASE KINASE; CHAIN: NULL;	ERK2; CHAIN: NULL;	ERK2; CHAIN: NULL;	TITIN; CHAIN: A, B;	GLUTATHIONE SYNTHETASE; CHAIN: A;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5.
SEQFOL D score			60.82			58.82				
PMF score	0.11	0.55		0.81	0.13		0.54	0.52	0.52	0.95
Verify score	-0.27	-0.31		0.03	-0.10		-0.27	-0.23	0.40	0.26
Psi Blast	1.1e-33	6.4e-34	1.6e-24	3.2e-43	1.1e-24		3.2e-27	0.0088	7.5e-07	9e-05
END	356	356	403	356	414	392	362	99	953	616
STAR T AA	148	150	42	127	162	83	150	E .	988	542
CHAI N ID		Ą		•			Ą	Ą	B	A
PDB ID	Ikoa	1 kob	1p38	1phk	Ipme	<u>ə</u>		2hgs	la9n	JL91
SEQ ID NO:	1724	1724	1724	1724	1724	1724	1724	1726	1728	1728

Γ.		T	T							_	_						Γ-										_		Γ-			
PDB annotation		REGULATION, RNP DOMAIN, RNA COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			RNA BINDING PROTEIN/RNA	NESTED DOUBLE PSEUDOKNOT	KINA STRUCTURE	RNA BINDING PROTEIN RNA- BINDING DOMAIN
Coumpound		R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*U)- CHAIN; P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*GP*UP*UP*UP* IIP*IIP*IID*IID*IID*IID*	ALPHA SPECTRIN; CHAIN: A,	В,С;				POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN I; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN I; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	UIA PROTEIN; CHAIN: A; HDV	RIBOZYME SELF-CLEAVED;	CITALIN. D,	HU ANTIGEN C; CHAIN: A;
SEQFOL	D score																		, page 6	(*************	****		***			- 1		-				3
PMF	score		0.43			0.10					1.00						0.57						0.43			`.			0.53			0.53
Verify	score		0.08			-0.04					0.10	•	_				0.47						0.54						-0.15			0.64
Psi Blast			3e-07			0.003					4.5e-05						7.5e-07					10	7.3e-07		_			1	6e-05		1	1.36-03
END	AA		856			835					612						956					0.00	220						614		13	014
STAR	t va		688			720					544						688					L C	/88						3		240)
CHAI		•	⊀			Ą					∢					Ī	<					t	τ,						∢			<
PDB	3		1b7f			1cm		2			[cA]		-				lcvj					T	[v]	•				1	OXO		1.10-	7001
SEQ	ğ Ş	_	1728			1728	74				1/28						1728					0.65	97/1				•		1728		1730	1720

PDB annotation	RNA BINDING PROTEIN RNA- BINDING DOMAIN	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN RNA BINDING PROTEIN RNA- BINDING DOMAIN		RIBONUCLEOPROTEIN PTB, PTB- C193, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
Coumpound	HU ANTIGEN C; CHAIN: A;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL:	NUCLEOLIN RBD1; CHAIN: A;	HNRNP A1; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A:	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POL YP YRIMIDINE TRACT. BINDING PROTEIN; CHAIN: A;
SEQFOL D score		٠						
PMF score	0.80	0.37	0.68	0.21	0.99	0.71	0.99	0.22
Verify	0.48	-0.23	0.65	0.48	0.42	0.32	0.13	-0.14
Psi Blast	3e-05	3e-06	1.5e-05	6e-07	1.5e-05	6e-07	1e-08	7.5e-05
END	598	835	614	947	612	614	946	614
STAR T AA	542	709	540	887	541	260	988	493
CHAI N ID	Ą	В		¥		A	Д	∢
PDB ID	149a	1dn1	1fht	1fj7	1ha1	1hd1	lnrc	Iqm9
SEQ ID NO:	1728	1728	1728	1728	1728	1728	1728	1728

	PDB annotation	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POL YPYRMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION	ļ	COMPLEX (RIBONUCLEOPROTEIN/RNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NIICI FAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA),
	Coumpound	POL YPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	UIA SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; IURN 6 RNA 21MER HARPIN (5'. (AP*AP*UP*CP*CP*AP*UP* 1URN 11 CHAIN: P, Q, R 1URN 13	MUSASHI1; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL:	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL:	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED
e de registro de seguir de la companya de la compan	SEQFOL D score					·		-	
	PMF	0.10	0.82	0,40	0.03	0.75	0.39	0.43	0.75
Read Albert Services	Verify score	0.10	0.51	-0.03	-0.03	0.18	0.42	0.05	0.51
Salar and Salar	Psi Blast	1.5e-07	0.0001	0.0001	1e-06	4.5e-06	3e-05	20 - 99	7.5e-07
	END	947	610	619	614	614	919	946	612
	STAR T AA	828	540	540	560	542	542	887	525
	CHAI N ID	V		4	4				4
,	PDB ID	Iqm9	1sx1	lum	2mss	2sxl	2ula	2u!a	2up1
	SEQ ID NO:	1728	1728	1728	1728	1728	1728	1728	1728
i						-		the second second second	

PDB annotation	HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A 1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RETENOMICT FOR A1	RNA BINDING DOMAIN, RBD, RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME	ENA BINDING DOMAIN RNA BINDING DOMAIN RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR. TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	PLASMA PROTEIN PLASMA PROTEIN, METAL-BINDING, LIPID- BINDING	
Coumpound	TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C,	SEX-LETHAL; CHAIN: A, B, C,	SERUM ALBUMIN; CHAIN: A;	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD
SEQFOL D score					-A	
PMF score		0.95	1.00	0.48	0.17	0.18
Verify score		0.32	0.58	0.38	-0.27	-0.46
Psi Blast	74.00	7.5e-07	.1e-05	3e-07	0.0015	1.16-28
END AA		947	612	958	336	347
STAR T AA		588 5	542	688	199	267
CHAI N ID		4	K	4	A	A.,
PDB		2up1	3sxl	3sxl	le7f	lahd
SEQ ID NO:		1728	1728	1728	1730	1733

PDB annotation		PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING	PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA	ULTRABITHORAX; PBX PROTEIN;	DNA BINDING, HOMEODOMAIN,	HOMEOTIC PROTEINS,	DEVELOPMENT, 2 SPECIFICITY		COMPLEX (DNA-BINDING	PROTEIN/DNA) DNA-BINDING	PROTEIN, DNA, PAIRED BOX,	TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING	PROTEIN/DNA) DNA-BINDING	PROTEIN, DNA, PAIRED BOX,	TRANSCRIPTION 2 REGULATION																
Coumpound	5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B:	DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC	PROTEIN IV; CHAIN: A;	HOMEOBOX PROTEIN	EXTRADENTICLE; CHAIN: B;	DNA (5'- CHAIN: C; DNA (5'-	CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B,	C; DNA; CHAIN: D, E, F			PAIRED PROTEIN; CHAIN: A, B,	C; DNA; CHAIN: D, E, F			TRANSCRIPTION REGULATION	TRANSCRIPTION FACTOR	LFB1 (HOMEODOMAIN) 1LFB3	GENE REGULATING PROTEIN	REPRESSOR PROTEIN FROM	BACTERIOPHAGE 434 (DNA-	BINDING IPRA 3 DOMAIN,	RESIDUES 1-69) (NMR, 20	STRUCTURES) 1PRA 4	GENE REGULATING PROTEIN	REPRESSOR (AMINO-	TERMINAL DOMAIN) (R1-69)	IR694	DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT
SEQFOL D score								. :												i													
PMF		0.07		0.46						0.92				9.1				0.99			0.51						0.78				0.19		
Verify score		-0.02		-0.12						-0.04				0.38				0.61			80.0						0.15				60.0		
Psi Blast		6.4e-24		6.4e-24						3.2e-23				9.6e-22				6e-24			0.00015			***************************************			0.0003				1.6e-26		
END AA		343		340						341				339				336			205						205				347		
STAR T AA		271		270						266				267				271			173						173				273		
CHAI N ID		Ą		¥						∢	,			щ																			
PDB ID		Z29I		158i			1			Ē				IŢI		1000		- QI			Ipra	·		_			1r69				Isan		
SEQ ID NO:		1733		1733						1733				1733				1733			1733						1733				1733		